us-09-327-750d-13.rni

```
1028 AATGGAAATGGCAGTGAGTACCGCACCTCCTGAAGGCTTTTGGCATCC 1077
                                                                                                                                                                           1078 GCTTCGACGTGCTGGTATACGGGAATGCTGGCAAGTTCAACATCATCCTCCC 1127
                                                                                                                                       676 GGACCGGGGGCGCGCGGGAGGAGGGCCCGGGACGATCCTCGGCCGC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          770 CCACCTCCGCCGCGCGCGCGCGCGCGCGGGGGGATCCGCGCGGGGG 819
                                                          94 MetGlyGluLeuSer.....98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 HisGlnGluAsnGluGluMetGluGlnProMet . . . GlnAsnGlyGluGl 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 uAspArgProLeuGlyGlyGlyGluGlyH1s.....GlnProA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 palaileProAsnArgGlnIleAsn.....AspGlyMetGlyG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
    Sequence 1, Application Us/07945283
    Fatent No. 535296
    GEREAL INFORMATION.
    APPLICANT: Neglecy Andrew K.
    APPLICANT: Neglecy Andrew K.
    TITLE OF INVENTION: peeudorables Virus Deletion Mutants
    TITLE OF INVENTION: Involving The EPO and LLT Genes
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-945-283-1
                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5215881-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores: 74 Quality: 77.50 Length: 74 Quality: 1.685 Gaps: 5 Percent Similarity: 62.162 Percent Identity: 35.135
                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
    Patent No. 251881
    Title OF INVENTION: PSEUDORABLES DIAGNOSIS PROBES INVENTION: SEQUENCES: 3
    CURRENT APPLICATION DATE:
    FILING DATE: 13-JUN-1990
    FILING DATE: 13-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: 5215881-2 from: 1 to: 2721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      820 GAGAAGGAGAGGAGGAG 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 lyAspGlyAspAspMetGlu 68
                                                                                                                                                                                                                                                           1128 ACCATCATCAGCTCTGT 1144
                                                                                                                                                                                                                          103 isHisAspGluPheCys 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-327-750D-13 x 5215881-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:2:
LENGTH: 2721
5215881-2
```

```
5 HisGingluAsnGluGluMetGluGinProMet...GlnAsnGlyGluGl 20 | Hiscill Hill | Hill |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 laGlyAsn.ArgArgGlyGlnAlaArgArgLeuAlaProAsnPheArgTr 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 uAspArgProLeuGlyGlyGlyGluGlyHis......GlnProA 33
                                                                                                                                                                                                                                                                                                             STATE: ILL
COMPUTER READALE FORM:
COMPUTER READALE FORM:
MEDILH TYPE: Floppy disk
COMPUTER: IS POF COMPATIBLE
COMPUTER: IN PC COMPATIBLE
SOFTAME: PRECEDIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 105/07/945,283
FILING DATE: 10920911
ATLASSIFICATION: 42
ATTORNEY ACENT INFORMATION:
NAME: RIADAGO, CULTIS P
REGISTRATION NUMBER: 309-66
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION
TELECOMMUNICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-07-945-283-1 from: 1 to: 8438
ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
CITY: Peoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEAVURE:

NAME/REY:
COSTON:
CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block;
US-09-327-750D-13 x US-07-945-283-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudorables virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variation
replace(1566, "c")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variation replace(7010, "g")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY

LOCATION

US-07-945-283-1
```

```
2368 CTGATCCGCTACAACGCCAAGCACGAGACCTGGACGTGCCCGGCACCGA 2417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: US-09-179-558-62 from: 1 to: 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::::!|||||||:::
730 AGCCTGCATCAGACCCCGGATTCCAAAACAGCTCCCCGAACACCACCA 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 InProhlaGlyAsnargArgGlyGlnalaArgArgLeuAlaProAsnPhe 47 in International Argonic Argo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          589 ......GAGGTCCTCGCGGTCGCCGAGGAGGTGGAGC 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              557 CATCGATACGGATGTG......CTGCACGCGCTTCCTCTAAGC 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AsnileHisGlnGluAsnGluGluMetGluGln.....Pr 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 ArgTrpAlalleProAsnArgGlnIleAsnAspGlyMetGlyGlyAspGl 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 yAspAspMetGluIlePheMetGluGluMetArgGluIleArgArgLysL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 euArgGluLeuGlnLeuArgAsnCysLeuArgIleLeuMetGlyGluLeu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-951-715A-6
                                                                                                                                                                                                                                                                                    alignment_scores: 163.50 Length: 103 Quality: 75.50 Gaps: 5 Brice 1.452 Gaps: 5 Percent Similarity: 50.485 Percent Identity: 25.243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-327-750D-13 x US-09-179-558-62/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: doub:
TOPOLOGY: linear
MOLECULE TYPE: Other
US-09-179-558-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 SerAsnHis 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         499 ... AACCAC 494
```

```
21 pArgProLeudlyGlyGlyGluGlyHisGlnProAlaGlyAsnArgArgG 38 This Control of the Cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2218 TTCAAGGAGAACTACGTGACCTGCCCGGCACCTTCAAGGAGTGCTACCC 2267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2318 GCTACCAGCTGCGCGGCTACATCGAGGACCAGGACCTGGAGATCTAC 2367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 lyGinAla.....ArgArgLeuAlaPro 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 alleProAsnArgGlnIleAsnAspGlyMetGlyGlyAspGlyAsp... 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 AsnPhe....ArgTrpAl 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 HisGinGluAsnGluGluMetGluGinProMetGlnAsnGlyGluGluAs 21
STATE: New York
COUNTRY: 305A
2.0F 1053
COMPUTER: 1810A
COMPUTER: 25.68P-1992
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PELEASILICATION: 900
PRIOR APPLICATION: 900
PRIOR APPLICATION DATA.
APPLICATION NUMBER: 105 07/72,027
PILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: SPULILI, W. MATERY
RESTREACE, DOCKET NUMBER: 22-943
RESTREACE, DOCKET NUMBER: 22-943
PREPERENCE, DOCKET NUMBER: 23-943
PREPERENCE, DOCKET NUMBER: 23-943
PREPERENCE, DOCKET NUMBER: 23-943
PREPERENCE, 1919-14-6615
INFORMATION INFORMATION: 6
SEQUENCE CHARACTERISTICS:
ILENGTH: 36-4 base pairs
TTPE: NUCLAIA PAGE PAIRS
TTPE: NUCLAIA PAGE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCATION: 1.3621 /product - Full-length, maize or the information: optmized cryile or the information: optmized cryile or the information: optmized cryile or the information: /note- bisclosed in Figure 6.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality: 75.50 Length: 147
Ratio: 1.198 Gaps: 7
Percent Similarity: 42.857 Percent Identity: 25.850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-07-951-715A-6 from: 1 to: 3624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Innear DESCRIPTION: Adesc - "Synthetic DNA" FEATURE: NO FEATURE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-327-750D-13 x US-07-951-715A-6
```

```
APPLICANT: Merlin, Ellis J.
APPLICANT: Adults, Karen L.
APPLICANT: Bounn. Cindy G.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE TATALON CONDUTION: USA
STREET: RACANALE SPORM:
MEDIUM TYPE: IN COMPATION OF SYNTHETIC DNA SEQUENCE TO SYNTHETIC DNA SECONDARY
APPLICATION NUMBER: US OF 7951,715
FILING DATE: 25-599-992
FILING DATE: 25-59
```

APPLICANT: Grossland, Lyle D,
APPLICANT: Wight, Martha S.
APPLICANT: Wight, Martha S.
APPLICANT: Wight, Martha S.
APPLICANT: Herlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Launis, Karen L.
APPLICANT: Bowman, Cludy G.
APPLICANT: Bowman, Cludy G.
APPLICANT: Dunder: Erik M.
APPLICANT: Dunder: Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Pace, Gary M.
APPLICANT: Pace, Gary M.
APPLICANT: SWITTE, MARTHER DUNGERED: SYMPHETIC DNA SEQUENCE HAVING ENHANCED NUMBER OF SEQUENCES: 94
CORRESPONDENCES: 95
CONTRESSEE: NO. 6075165artis Corporation
STREET: 3054 Cornvallis Road
CITY: Research Triangle Park
COUNTY: USA
COMPUTER: Enhance FORM:
MEDIUNY TPE: Floppy disk
MEDIUNY TPE: Floppy disk
MEDIUNY TPE: Floppy disk
COMPUTER: TEN PC COMPATI:
MEDIUNY TPE: PLOPPY disk
MEDIUNY TPE: PLOPPY disk
COMPUTER: TEN PC COMPATI:
MEDIUNY TPE: PLOPPY disk
MEDIUNY TPE: PLOPPY TPE: 2218 TTCAAGGAGAACTACGTGACCTGCCCGGCACCTTCAACGAGTGCTACCC 2267 2268 CACCTACCTGTACCAGAAGATCGGCGAGAGCGAGCTGAAGGCCTACACCC 2317 2318 GCTACCAGCTGCGCGGCTACATCGAGGACAGCCAGGACCTGGAGATCTAC 2367 2368 CTGATCCGCTACAACGCCAAGCACGAGACCCTGGACGTGCCCGGCACGA 2417 38 lyGlnAla.....ArgArgLeuAlaPro 45 46 AsnPhe.....ArgTrpAl 50 50 alleProAsnArgGlnIleAsnAspGlyMetGlyGlyAspGlyAsp.... 65 68 GluilePheMetGluGluMetArgGluileArgArgLysLeuArgGluLe 94 seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-08-459-504B-6 93 .. LeuMet.GlyGluLeuSerAsnHisHisAspHisHis 104 seq_documentation_block:
; Sequence 6, Application US/08459504B
; Patent No. 6075185 SEMERAL INFORMATION:
APPLICANT: KOZIGI, MICHAEL G.
APPLICANT: DEMAI, MAINI M.
APPLICANT: KTAMEY, VANCE C.
APPLICANT: KTAMEY, VANCE C.
APPLICANT: WARTEN, GREGOTY W.
APPLICANT: EVOID, Stephen V.
APPLICANT: CROSSLAND, LYLE

		21 2167	38 2217	45	50	65 2367	29	2417	84	92 2517	
Length: 147 Gaps: 7 Percent Identity: 25.850	14-6 1-6 from: 1 to: 3624	HisdindluasnGludluMetGludinProMetGlnAsnGlyGludluas	pargproteudlydlydlygludlytisglnbroaladlyasnargargg 38 :::	1ydlablahrghrgfeuhlabro ::: ::: rrcabggaaactacgrgaccrgcccggcacctrcacgaggagctacc	ASDPHEAEGTrPAL 50 ::::: CACCTACCTGACGGAGGGGGGGGGGGGGGGGGGGCGTAAGGCCTACACCC 2317	allerroksnargdinileksnaspdiymetdiydiyaspdiyksp 65 ::! ::::::	AspMet	CTGATCCGCTACAACGCCAAGCACGAGACCCTGGACGTGCCCGGCACCGA 2417	GlullePheMetGluGluMetArgGlulleArgArgLysLeuArgGluLe 84	84 uGinLeukrgAsnCysLeukrgile	nHisHisAspHisHis 104
Quality: 75.50 Ratio: 1.198 Percent Similarity: 42.857 Pe	0S-09-327-750D-13 x US-08-459-444-6 Align seg 1/1 to: US-08-459-444-6 from: 1					alleProAsnArgGln1leAsnAs ::: GCTACCAGCTGCGGGCTACATCG				uGlnLeuArgAsnCysLeuAr 	93Leuwet.GlyGluLeuSerAsnHisHisAspHisHis 104
Percent	OS-09-3	5 2121	21 2168	38	46	2318	99	2368	68 2418	84 2468	93

```
The present invention relates to a purified polypeptide capable of binding memorrophin receptor (p7-4RR). The invention is useful for binding and modulating the activity of p75kRs. The peptide mediates MFF-indened apopticals, which plays an important role in meurogenetic diseases. The peptide of the invention and p75kRs are useful for inhibiting NF-kappes activation in a cell or a subject, for inducing caspase-2 and caspase-3 activity to cleave poly (ADF-ribose) polymerase and fragment nuclear DNA in a cell by co-expression of (1) and p75-WRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New p7s-neurotrophin receptor-associated cell death executor (NADS) at the gene encoding NADS, useful for modulating the activity of p75NTR and for detecting neurodegenerative diseases .
   20000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.00
80.00
80.00
79.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetAlaAsnileHisGlnGluAsnGluGluMetGluGlnProMetGlnAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 lyAsnArgArgGlyGlnAlaArgArgLeuAlaProAsnPheArgTrpAla 50
                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF23529
                                                                                                                                                                                                                                                                                                                                                                                                                   Neurotrophin receptor; p75-NTR; NGF-induced apoptosis; neurogenetic disease; NF-kappaB; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 891 BP; 251 A; 182 C; 224 G; 234 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SIDSZ/gcgdatz/geneset/geneseqt/Nk2001 bbr; AAD04966
SIDSZ/gcgdatz/geneset/geneseqt/Nk2001 bbr; AAD04966
SIDSZ/gcgdatz/geneseqt/geneseqt/Nk2001 bbr; AAD04964
SIDSZ/gcgdatz/geneseqt/geneseqt/Nk2001 bbr; AAD04964
SIDSZ/gcgdatz/geneseqt/geneseqt/Nk201 bbr; AAA11288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AAF23529 from: 1 to: 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 134pp; English.
                                                                                                                                                                                    sed_documentation_block:

ID AAF23529 standard; DNA, 891 BP. XX
AAF23529;
XX Z 2-MAR-2001 (first entry)
XX X B Human NADE DNA.
XX Neurotrophin receptor; p75-WTR; N Neurotrophin receptor; p75-WTR; N Neurotrophin sapiens.
XX HO200075278-A2.
XX NO200075278-A2.
XX NO-JUNI-1999; 990S-0327750.
XX NOS-JUNI-1999; 990S-0327750.
XX The present invention receptor (P7 Dinding and modulating the activity NGF-induced approals, which play CC diseases. The peptide of the invention of complete and cappage 3 cutylity CC Cappase 2 and caspase 3 cutylity CC Cappase 2 and caspase 3 cutylity CC CASPASE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-327-750D-13 x AAF23529
                                                                                                                                                                                    About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
      out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secore List:
Secore List:
Secore List:
Settd Orig 25core EScore Len |
SID52/gcgdata/geneseq/yRAX000.DAT:AAR23129 +
SID52/gcgdata/geneseq/yRAX000.DAT:AAR23128 +
SID52/gcgdata/geneseq/yRAX000.DAT:AAR23128 +
SID52/gcgdata/geneseq/yRAX000.DAT:AAR312128 +
SID52/gcgdata/geneseq/yRAX000.DAT:AAR31212 |
SID52/gcgdata/geneseq/yRAX000.DAT:AAR31212 |
SID52/gcgdata/geneseq/yRAX000.DAT:AAR31213 |
SID52/gcgdata/geneseq/yRAX000.DAT:AAR31313 |
SID52/gcgdata/geneseq/yRAX000.DAT:AAR3131 |
SID52
OM of: US-09-327-750D-13 to: N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search information block:
Query: US-09-1277-50D-13
Query: US-09-1277-50D-13
Database: UGenesag-1101:
Database sequences: 930621
Barbase length: 455566000
Search time (sec): 355.560000
                                                 Date: Mar 11, 2002 3:42 PM
                                                                                                                                                                       Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     score_list:
Sequence
/SIDS2/qcqdat
```

07-JUN-1999; 99US-0327750.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

Homo sapiens. EP1033401-A2. 06-SEP-2000.

Human secreted protein 5' EST, SEQ ID NO: 1003.

06-OCT-2000 (first entry)

```
New p75-neurotrophin receptor-associated cell death executor (NADE) and
the gene encoding NADE, useful for modulating the activity of p75NTR
and for detecting neurodegenerative diseases
                                                                                                                                                                                           The present invention relates to a purified polypeptide capable of binding neucotrophin receptor (p75-WRN). The invention is useful for binding and modulating the activity of p75WRN. The peptide mediates MGF-Induced apopticals, which plays an important role in meurogenetic diseases. The peptide of the invention and p75WRN are useful for inhibiting NF-kappas activation in a cell or a subject, for inducing caspase-2 and caspase-3 activity to cleave poly (ADP-ribose) polymerase and fragment nuclear DNN in a cell by co-expression of (1) and p75-WRN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 lyasn.....ArgArg 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 gGlnIleAsnAspGlyMetGlyGlyAspGlyAspAspMetGluIlePhem 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC01005
                                                                                                                                                                                                                                                                                                                          Sequence 700 BP; 177 A; 188 C; 203 G; 132 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAF23528 from: 1 to: 700
                                                                                                                                                                Claim 12; Fig 1; 134pp; English
                        (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sAspGluPheCysLeuMetPro 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    527 TGATGAATTCTGCCTTATGCCT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-327-750D-13 x AAF23528
                                                                              WPI; 2001-061707/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104
```

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'85's and for diagnostic, Coresto, gene therapy and chromosome mapping procedures

Dumas Milne Edwards J, Duclert A, Giordano J;

(GEST) GENSET.

WPI; 2000-500381/45. P-PSDB; AAG00999.

21-FEB-2000; 2000EP-0200610. 26-FEB-1999; 99US-0122487

```
The present sequence is one of a large number of 5' ESTS derived from menhas encoding secreted proteins. An ORP has been identified within the sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oilgo-dr prinade CDNA ilbraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. So for the formal submitted on the second on the sequence of the sequence in the cDNAs and cDNAs are set of the full sequences and the full sequence in the second of the sequences of the sequence of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 IleProAsnArgGlnIleAsnAspGlyMetGlyGlyAspGlyAspAe 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 532 BP; 151 A; 121 C; 163 G; 91 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 1003; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAC01005 from: 1 to: 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-327-750D-13 x AAC01005
```

seq_documentation_block: ID AAC01005 standard; cDNA; 532 BP. XX

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss

Homo sapiens. EP1074617-A2. 07-FEB-2001.

```
comprises: (a) an oligo-dry primer and an oligonuclectide complementary controllectide sequences defined in the specification. Where a primer and an oligonuclectide complementary strand of a polynuclectide which comprises one of the SGD nuclectide sequences defined in the specification, where the oligonuclectide comprises at least 15 nucleotides; or (b) a combination of an oligonuclectide comprises at least 15 nucleotides; or (b) a combination of sequence and an oligonuclectide comprises a $i$-end a polynuclectide comprises a $i$-end a sequence and an oligonuclectide comprises a $i$-end comprises at least 15 nucleotides and the combination of the $j$-end sequence; or oligonuclectide comprises a $i$-end sequence and an oligonuclectide comprises at least 15 nucleotides and the combination of the $j$-end sequence; or oligonuclectide which comprises at least 15 nucleotides and the combination of the specification. The primers are useful for spitesisting bolynucleotides, particularly full-length CDMAs. The primers are useful for spites stating polynucleotides, particularly full-length CDMAs. The primers are also useful for the comprise as a seally without any specialised methods. Admittaged to Admittage and Admittages and
```

Sequence 865 BP; 239 A; 177 C; 224 G; 221 T; 4 other;

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J; Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

29-JUL-1999; 99JP-0248036. 27-AUG-1999; 99JP-0300253. 11-JAN-2000; 2000JP-0118776. 02-MAX-2000; 2000JP-018376. 09-JUN-2000; 2000JP-0241899.

(HELI-) HELIX RES INST.

WPI; 2001-318749/34.

28-JUL-2000; 2000EP-0116126

```
67 tGluilePheMetGluGluMetArgGluileArgArgLysLeuArgGlui 84
430 AGAAAGGTTTG:20GGCGAATGArGGAACAACAAGAAAAAACAAGGAAC 479
                                                                                                                                                                                                      84 euGlnLeuArgAsnCysLeuArgIleLeuMetGlyGluLeuSerAsnHis 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AsnileHisGlnGluAsnGluGluMetGluGln...ProMetGlnAsnGl 18
                                                                                                                                                                                                                                                                                                                           35 sn...ArgArgGlyGlnAlaArgArgLeuAlaProAsnPheArgTrpAla 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH13750
alignment_scores:
Quality: 277.00 Length: 111
Ratio: 3.298 Gaps: 4
Percent Similarity: 75.676 Percent Identity: 54.955
                                                                                                                                               Align seg 1/1 to: AAH03517 from: 1 to: 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        530 TATGAC.....TITTGCCTCATACCT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 HisAspHisHisAspGluPheCysLeuMetPro 111
                                                                                       alignment_block:
US-09-327-750D-13 x AAH03517
```

Human cDNA sequence SEQ ID NO:10656

```
The present invention describes primer sets for synthesising 5602

(All-length Conbus defined in the specification, Where a primer set

(All-length Conbus defined in the specification, Where a primer set

(Comprises: (a) an oilgoud primer and an oilgonucleotide complementary

(COMPLISES: (a) an oilgoud primer and an oilgonucleotide complementary strand of a polynucleotide which comprises one of

(COMPLISES: (b) an oilgonucleotide comprising a sequence complementary to the

(COMPLISES: (b) an oilgonucleotide comprising a sequence complementary to a

(SOM) sequence and an oilgonucleotide which comprises a 5'-end

(SOM) sequence and an oilgonucleotide sequence, where the

(COMPLISES: (c) and sequence as a 1'-end sequence where the

(COMPLISES: (c) and sequence as a 1'-end sequence where the

(c) ingonucleotide which comprises a 1'-end sequence (c) primers as a 1'-end sequence (c) primer sets can be used in antisense therapy and

(C) the 5'-end sequence as elected from those defined in

(C) the formation of the primers are also useful for the

(C) dene therapy. The primers are useful for synthesising polyuncleotides,

(C) the full-length cDNAs. The primers are also useful for the

(C) defined assaily without any specialised methods. AMR03646 to

(C) AMR03893 represent human amino acid sequences; AM803466 to

(AM803893 represent human amino acid sequences; and AM13632

(C) fethe present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 yGluGluaspargProLeuGlyGlyGluGlyHisGlnProAlaGlyA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 AsnileHisGluGluAsnGluGluMetGluGln..ProMetGlnAsnGl 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1229 BP; 351 A; 243 C; 296 G; 339 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality: 277.00 Length: 111
Ratio: 3.298 daps: 4
Percent Similarity: 75.676 Percent Identity: 54.955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; SEQ ID 10656; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAH13750 from: 1 to: 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-327-750D-13 x AAH13750
```

```
The present sequence is the coding sequence for a human brain-expressed X-linked protein (DBRA). Hex and its coding sequence are useful in the diagnosis and treatment of dysembryoplasis, hereditary diseases, cancer, tunours, deafness, X-chromosome-binding mental retradition and lissencephalous disease. Hex is also useful for screening minute, adonts, or inhibitors, and in peptide fingerprinting identification. Hex coding sequence can be used as primers or probes, or in producing gene chips or microarrays.
                                                                                    Isolated human brain-expressed Y-linked polypeptide used to diagnose and treet of dysembryphasts, hereditary diseases, cancer, tumor, deariness and X-chromosome-binding mental retardation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; X chromosome linked gene expression protein 14; cancer;
                                                                                                                                                           Claim 5; Page 22; 30pp; Chinese
                                 WPI; 2001-397944/42.
P-PSDB; AAB99224.
Mao Y, Xie Y;
  AAA87080 to AAA87656 represent nucleic acid sequences (NI) encoding a acariongenesis biomarkers, the carcinogenesis biomarkers are induced by treating rat hepatocytes with phenobarbitol. The nucleic acids are useful for identifying carcinogenic compounds. The nucleic acid molecules can be used to derive probes and/or primers for detecting or inducing carcinogenesis, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; brain expressed X-linked procein; cytostatic; auditory; nootropic; hisex; dysembryoplasia; hereditary disease; cancer; tumour; deafines) X-chiromsome-binding mental retardation; lissencephalous disease; ss.
                                                                                                                                          New nucleic acid encoding a carcinogenic biomarker, induced by enchembarbitol treatment of rat hepatocoytes, useful for identifying charchostic compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed X-linked protein, hBex, coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 IleargargLysLeuargGluLeuGlnLeuargasnCysLeuargIleLe 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ATCCGGAGAAAGCTTAGGGAGCTGCAGTTGAAATTGTCTGCGTATTCT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH45143
                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores: 193.00 Length: 35 Caparity: 193.00 Gaps: 0 Ratio: 5.514 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                              Sequence 187 BP; 39 A; 48 C; 40 G; 60 T; 0 other;
                                                                        Bunch RT, Curtis SW, Rodi CP, Morris DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAA87147 from: 1 to: 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.
                                                                                                                                                                                                              Claim 1; Page 73; 240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID AAH45143 standard; cDNA; 792 BP.
99US-011807B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-NOV-2000; 2000WO-CN00502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-327-750D-13 x AAA87147
                                    (SEAR ) SEARLE & CO G D.
                                                                                                        WPI; 2000-505977/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W0200140286-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 etPro 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 recer 106
29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH45143;
```

```
Human X chromosome linked gene expression protein 14 coding sequence.
                                                                                                                                                                                                                                  212 AIGGAAATGCCAACCAAGAAAATGAAGAAAAGGAGGAAGTIGCTAATAA 261
                                                                                                                                                                                                                                                                                                        262 AGGGAGCCCTTGGCCCTTGGATGCTGGTGATACTGTGTGCTA 311
                                                                                                                                                                                                                                                                                                                                                                       412 GAATATGGAAAGGATTGGGGAGGGGGTGAGACAGCTGATGGAAAAGCTGA 461
                                                                                                                                                                                                                                                                               17 nGlyGluGlu. . AspArgProLeuGlyGlyGlyGluGlyBisGlnProA 33
                                                                                                                                                                                                                                                                                                                                                 33 laGlyAsnArgArgGly...GlnAlaArgArgLeuAlaProAsnPheArg 48
                                                                                                                                                                                                                                                                                                                                                                                                                  49 TrpAlaileProAsnArgGlnIleAsnAspGlyMetGlyGlyAspGlyAs 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 paspMetGluIlePheMetGluGluMetArgGluIleArgArgLysLeuA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 rgGluLeuGlnLeuArgAsnCysLeuArgIleLeuMetGlyGluLeuSer 98
                                                                                                                                                                                                                  1 MetalaAsnileHisGlnGluAsnGluGluMetGluGlnProMetGlnAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seg_name: /SIDS2/gcgdata/geneseg/genesegn/NA2001.DAT:AAH75810
Sequence 792 BP; 214 A; 172 C; 219 G; 187 T; 0 other;
                                                 Align seg 1/1 to: AAH45143 from: 1 to: 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-327-750D-13 x AAH45143
```

Page

```
Claim 5; Page 181-182; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
IID AAC03880 standard; cDNA; 662 BP.
XX
AC AAC03880;
XX
XX
          Human cell cycle and proliferation protein CCYPR-22 cDNA, SEQ ID NO:76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cell cycle and proliferation proteins and polynuclectides are used to treat, dispance and prevent famine, developmental and cell signaling disorders and cell proliferative disorders including cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell cycle and prollferation protein; CCYPR; human; agonist; antagonist; gene tharay; detection; gene therapy; transgenic animal disease model; immune disorder; developmental disorder; cell signalling disorder; excell prollferative disorder; cancer; tumnour; anamia; epilepsy; arteriosiclerosis; asthma; allergy; diabetes mellitus; menstrual cycle disorder; bacterial infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yue H, Au-Young J, Bandman O;
Baughn MR, Patterson C, Shah P;
                                                                                                                                                                                                                                    16 nasnGlydluGlu...AspargProLeuGlyGlyGlyGlyGluGlyH18GlnP 32 | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | ::11| | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 AGATGGGACATAATGCATAGGCTTGGAGAGCCACAGGCAAGGATGAGAGA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         521 TGAGGGAAAAGCAGTTGAGTCATAGTTTGCGGGCAGTCAGCACTGAT... 567
                                                                                   3 AsnileHisGlnGluAsn.....GluGluMetGluGlnProMetGl 16
                                                                                                                                                                                                                                                                                                                                                                                                32 roalaGlyAsnArgArgGly...GlnAlaArgArgLeuAlaProAsnPhe 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 ArgTrpAlaileProAsnArgGlnIleAsnAspGlyMetGlyGlyAspGl 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 euArgGluLeuGlnLeuArgAsnCysLeuArgIleLeuMetGlyGluLeu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF59611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     568 CCCCCTCACCATGACCATCACGATGAGTTTTGCCTTATGCCC 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 SerAsnHisHisAspHisHisAspGluPheCysLeuMetPro 111
     Align seg 1/1 to: AAI58581 from: 1 to: 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID AAF59611 standard; cDNA; 898 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT,
Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0145075.
99US-0153129.
99US-0164647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-2000; 2000WO-US19948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-112727/12.
P-PSDB; AAB60474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillman JL, Lal P,
Azimzai Y, Yang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200107471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1999;
08-SEP-1999;
10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF59611;
```

```
Sequences AAF5950-AAF59643 represent CDNAs encoding 54 human

cell cycle and proliferation proteins (CCFPR, AAB60645-AAB60506.

CCTPR and agonists of CCPPR are used to treat diseases or conditions.

CCTPR and agonists to CCTPR are used to treat diseases or conditions.

CCTPR and agonists to creat diseases or conditions associated with antegorists are used to enranelinked immunosorben associated with a core expression of functional CCPPR. Monoclonal or polyclonal antibodies to corp may be used in enranelinked immunosorben associated with a conditional color and the core and provided in a conditional antibodies.

CC radioimmunosasys to detect CCPPR. CCPPR itself may be used to detect compounds etg., antibodies, oligomiclectides and proteins (receptors) (cc that specifically bind to CCYPR. and in drug screening methods to inclectides can be used to generate transgenic animal models of human disease, and can be used to generate transgenic animal models of human concentralities with respect to the expression of CCYPR. CCYPR canomical in the confidence and prevented with CCYPR. Diseases which can be disponder associated with CCYPR. Diseases which can be disponder associated with CCYPR. Corper and colorents and cell and cell signalling disorders and cell proliferative developmental and cell signalling disorders and cell proliferative concerting and collections and collections and collections and collections and collections and cell signal and cell advancer. Specific examples of these disorders and infections caused by bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 AATGTCAACCAGGAAAATGATGAAAAGAAGAAAAGGAGGAAGTTGCTAA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         499 GGAGAATATGGAAAGGATTGGGGAGGAGGTGAGAAGACAGAAAGC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 yAspAspMetGluIlePheMetGluGluMetArgGluIleArgArgLysL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 roAlaGlyAsnArgArgGly...GlnAlaArgArgLeuAlaProAsnPhe 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 ArgTrpalalleProAsnArgGlnIleAsnAspGlyMetGlyGlyAspGl 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 euargGluLeuGlnLeuArgAsnCysLeuArgIleLeuMetGlyGluLeu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AsnileHisGlnGluAsn......GluGluMetGluGlnProMetGl 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC03880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 898 BP; 250 A; 186 C; 251 G; 211 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 114
Gaps: 4
Percent Identity: 41.228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAF59611 from: 1 to: 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality: 175.00
Ratio: 2.465
Percent Similarity: 62.281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11ignment_block:
US-09-327-750D-13 x AAF59611
```

US-09-327-750D-13 x AAC10889

Align seg 1/1 to: AAC10889 from: 1 to: 692

```
5077
682
436
108
1294
8 - 76.50 120.21 47.95

1-8 - 76.50 117.25 70.14

12 - 76.50 134.65 753

47 - 76.00 132.90 9.42

2 + 76.00 132.90 9.42
                                                                                                                                                                                                                  Sequence 1. Application PC/TUS9206840

Sequence 1. Application PC/TUS9206840

GENERAL INFORMATION: Shi, Yang
PPLICANT: Serio, Edward

APPLICANT: Shi, Yang

APPLICANT: Shi, APPLICANT: AND

APPLICANT: Shi, APPLICANT: AND
                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/1na/PCTUS_COMB.seq:PCT-US92-06840-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 86
Gaps: 3
Percent Identity: 29.070
        alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMAND 110e parameters:
-HODEL-framet-pf. model - DEV-x1h
-HODEL-framet-pf. model - SEV-x1h
-HODEL-framet-pf. model - SEV-x1h
-DB-12-pf. model - DEV-x1h
-DB-12-pf. model - DB-12-pf. model - DEV-x1h
-DB-12-pf. model - DB-12-pf. model - D
            OM of: US-09-327-750D-12 to: Issued_Patents_NA:* out_format : pfs
                                                                                                                              About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search information block:
Ouery 105-09-127-7500-12
Ouery 105-09-127-7500-12
Ouery 15sted_1atents_NA:
Database sequences: 35120
Search time (sec): 146.09000
                                                                   Date: Mar 11, 2002 3:36 PM
```

```
NAME/KEY:
DOGATION:
NATION:
NATIONS: NASSABLIMA, MATIKO, et al.
AUTHORS: NASSABLIMA, MATIKO, et al.
TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester tr.
VOURNAL: 39 Lipid Res.
1SSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARICAMY: "Treat" 11. ".
APPLICAMY: "Treat" 11. ".
APPLICAMY: "Treat" 11. ".
APPLICAMY: "BLOSYNTHON: Production
FITHE OF INVENTION: Production
FORESPONDENCE: 39
CONTESPONDENCE: 39
ADDRESSE: Dow ANGROSCIANCE ILC Patent Department
STREET: 93.0 Islantile Road
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 GACGTCAGCGGCGAGAGGGCCGTGATGCTCCTCGGCCGGGTCAAGTACGG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 TGGAGCTGGTGGACGCCAAGACCATCGACGTCGCCATCCAGAACGTGTCC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 rgGluIleArgArgLysLeuArgGluLeuGlnLeuArgAsnCysLeuArg 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 AAGAGGGCCAAGGTGGTCCAGACGCCTTCCAGCGCGCCGGCTATCCG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 HisGlnGluAsnGluGluMetGluGlnProLeuGlnAsnGlyGluGluAs 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 pargProValGlyGlyGlyGlyGlyH1sGlnProAlaGlyAsnAsnA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 snAsnAsnHisAsnHisAsnHisAsnHisHisArgArgGlyGlnAlaArg 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 ArgLeuAlaProAsnPheArgTrpAlaIleProAsnArgGlnMetAsnAs 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 pdlyLeuglyGlyAspAspAspMetGluMetPheMetGluGluMetA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgr2_5/ptodata/2/ina/6A_COMB.seq:US-09-036-987A-1
                                                                                                                                                                                                                                                                                                                                                                                       PAGES: 1643 - 1649

DATE: 1988

RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1488
US-09-171-969-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:

Quality: 81.00
Quality: 1.373
Percent Similarity: 58.416
Percent Identity: 28.713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-09-171-969-1 from: 1 to: 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_plock:
    Sequence 1, Application US/09036987A
    Patent No. 6143526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-327-750D-12 x US-09-171-969-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 GTT 32C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 Ile 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:

Sequence 1, Application US/09171969

Sequence 1, Application

Sequence 1, Application

Farence 1, Sequence 3,

TITLE OF INVENTION:

CORRESONERNCE S.

CORRESONERNCE ADDRESS:

ADDRESSEE Banner Witcoff Ltd.

STREET: 75 State Street, Suite 2300

STATE: Masschusetts

COMPURY: USA

COMPURY
554 CAGICCAAGCGCCTCGTCGTCACGTCGACAGCTCTCGAAGCGCGA 603
                                                                                                                                                                                                                                                                                                                                                                                             654 TCGAGCGCACCCCGGGAAGTTCACCAAGCTGATCTCCCGGCGGCGACGCG 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             704 ATCTACTCCAGCACGGACGCTGCTCGCTTCGACGTCCGCAGCGG 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 laIle.....ProAsnArg...GlnMetAsnAspGlyLeu...GlyGly 75
                                                                                                                                                                                                                                                                                                            76 AspGlyAspAspMetGluMetPhemetGluGluMetArg......88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 .....GluileArgArgLysLeuA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-171-969-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSICTATION THAY 1397 (01.03.97)

PRICESTORY OF THE TABLE TO THE TABLE THE THE TABLE THE THE TABLE THE TABLE THE TABLE THE TABLE TO THE TABLE TABLE THE TABLE THE TABLE THE TABLE THE TABLE THE TABLE TABLE THE TABLE THE TABLE THE TABLE TABLE THE TABLE TABLE TABLE TABLE THE TABLE TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
FEATURE: Structural coding sequence for
FEATURE: mature rabbit CETP
```

us-09-327-750d-12.rni

```
280623 AGCAGGCCGACGTTCCGGCCATCAGTGCCGGTGCGGCGAACCGAACCGC 280672
     95 rgGluLeuGlnLeu.....ArgAsnCysLeu......Arg 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:

OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "1" bases at various positions throughout the sequence;
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                       APPLICARY: FIGERBAN, ROBERT D.
APPLICARY: HITE, Owen R.
APPLICARY: HITE, Owen R.
APPLICARY: PARER, Claire M.
APPLICARY: PERSER, Claire M.
APPLICARY: PERSER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERREC: 1466-2000/100
CURRET APLICARION NUMBER: US/09/103,840A
CURRET APLICARION NUMBER: US/09-06-24
NUMBER OF SEQ 10 NOS: 2
SOFTWARE: Patentin Ver: 2.1
SEQ 10 NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280423 TACCGGCGATAGCGCCCACGATTGGCCGGCCGGCTCGCTTCCGGTCAGC 280472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280323 CCGGTGACGGGGGTGCTGACCGGGGGTCCAGATCGGCCGACGGCATAAC 280372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280373 GATGAACGGGTCGCCCCCGAGCTCGAGCACGGTCGGCTTGATCTCGT 280422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280523 GCTAACAAGCAACGTCTGGAAGCAGCCGTCCGGGAAGCCGCCTCGGGGA 280572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 laGlyAsnAsnAsnAsnAsnAsnHis......AsnHisAsn 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 HisGlnGluAsnGluGluMetGluGlnProLeuGlnAsn...GlyGluGl 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 rgTrpAlalleProAsnArgGlnMetAsnAspGlyLeuGlyGly..... 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 paspMetGluMetPheMetGluGluMetArgGluIleArgArgLysLeuA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 HisHisArgArgGlyGlnalaArg..... 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 .....AspGlyAs 78
                                                                seg_name: /cgn2_6/ptodata/2/ina/6B_COMB.seg:US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-09-103-840A-2 from: 1 to: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
Quality: 80.00
Quality: 0.03
Quality: 48.171
Percent Similarity: 48.171
Percent Identity: 23.171
69116 GCTGCACACGTCACCACCACAGACGTGCCTC 69085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FE: DNA
RGANISM: Mycobacterium tuberculosis
                                                                                                        seq_documentation_block:
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-327-750D-12 x US-09-103-840A-2
```

```
APPLICANT: HISTOCHANA, ROBERT D.
APPLICANT: WHITE, OWDER R.
APPLICANT: WHITE, OWDER R.
APPLICANT: WHITE, OWDER, CLAILE W.
APPLICANT: VERYER, CLAILE W.
TILLE OF INVENTION: UTBERCULLOSIS
TILLE REPRENCE: 24366-24000.00
CURRENT APPLICANTON WOMBER: 1950-924
CURRENT APPLICANTON WOMBER: 1950-6-24
SEQ ID NO: 2
SEQ ID NO: 2.1
SEQ ID NO: 2.1
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280260 GATGAACGGGTCGCTGCCGCCCGAGCACGGTCGGCTTGATCTCGT 280309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280310 TACCGGCGATAGGCCCACCGATTGGCCGGCCGGCTCGCTTCCGGTCAGC 280359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280160 CGATGAACGGCTTGGCGGCGATGCAGGATTGGCCGTTGTTCTGCACCCG 280209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280410 GCTAACAAGCAACGTCTGGAAGCAGCCGTCCGGGAAGCCGCCTCGGGCGA 280459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 uAspArgProValGlyGlyGlyGluGly.....HisGlnProA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 laGlyAsrAsoAsoAsoAsoAsoRis.....AsoHisAsoHisAso 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 HisHisArgargGlyGlnAlaArg..... 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 rgTrpAlalleProAsnArgGlnMetAsnAspGlyLeuGlyGly.....75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 HisGlnGluAsnGluGluMetGluGlnProLeuGlnAsn...GlyGluGl 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 .....ArgLeuAlaProAsnPheA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 .....AspGlyAs 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PASPMetGluMetPheMetGluGluMetArgGluIleArgArgLysLeuA 95
                                                                                              seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-103-840A-1
                                  280673 TIGCCACAGGGGAAGTICCATGCCATCACCCCAGGATCAC 280714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-09-103-840A-1 from: 1 to: 4411529
105 IleLeuMetGlyGluLeuSerAsnHisHis .....AspHis 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores;

Quality: 80.00

Ratio: 1.013

Percent Similarity: 48.171

Percent Identity: 23.171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1
                                                                                                                                          seq_documentation_block:
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-327-750D-12 x US-09-103-840A-1
```

us-09-327-750d-12.rni

; OTHER INFORMATION: UTH4 US-09-323-433A-3

```
seq_documentation_block:
Sequence 3 Application US/09323433A
Patent No. 6218512
GENERAL HERORAATION:
GENERAL HERORAATION:
APPLICANT: Guatence, Leonard P.
APPLICANT: Gold-granced Jr., Nicanor
APPLICANT: Cole, Francesca
APPLICANT: Cole, Francesca
APPLICANT: Cole, Francesca
APPLICANT: Cole, Francesca
APPLICANT: NewTYDN: GENES DETERMINING CELLULAR SENESCENCE IN
TITLE OF INVENTYON: TREAD
TITLE OF INVENTYON: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2533 ATAACAATAATAATCAAAAGAGTCATACCCGTCATTTTTCTTTACAGCT 2582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2483 TAGTCATAATCATAATCATAATCATAATCATAACCATGCTCACAATAATA 2532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 ......AsnargdlmaetasnaspdlyLeudlydlyaspdlyaspas 79
2583 AargcTracthallis: Ullinistics
2583 AargcTracthalachachachachachacharath...... 2624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2451 AACAACGAAAATAAGAACCCC......CATAACAAAAA 2482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2625 .....Trctcaaccaatatg......cacaagatcaga 2652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 aGlyAsnAsnAsnAsnAsnHisAsnHisAsnHisAsnHisHisArgA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 pMetGluMetPheMetGluGlu MetArgGluIleArgArgLysLeuArg 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 AsnGlyGluGluAspArgProValGlyGlyGlyGluGlyHisGlnProAl 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 rgGlyGlnAlaArgArgLeuAlaProAsnPheArgTrpAlaIlePro... 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-323-433A-3
                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores: 1.362 Length: 92 Gaps: 5 Retion 1.362 Gaps: 5 Percent Similarity: 63.043 Percent Identity: 26.087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-396-001-3 from: 1 to: 3455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 GluLeuGlnLeuargAsnCysLeu 103
::::: |||||||| |||
2653 AAATTCACTCTCGGCAACAATTA 2676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
us-09-327-750D-12 x us-08-396-001-3
TOPOLOGY: linear
NOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 663.3164
US-08-396-001-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (663)...(3164)
```

```
GENERAL INCURANION, Stephen L.
APPLICANT: Heditan, Stephen L.
APPLICANT: Heditan, Richard C.
APPLICANT: Heditan, Richard C.
APPLICANT: Heditan, Richard C.
APPLICANT: Heditan, M.Chard C.
APPLICANT: Gedegah, Martha TITLE CF TIVERFILD POLYNOLEDTIDE VACCINES
TITLE CF TRVENTION: POLINGLEAR, METHODS CP PROFECTION AND VECTOR FOR TITLE CF TRVENTION: DELIVERING POLYNOLECTIDE VACCINES
TITLE CF TRVENTION: DELIVERING POLYNOLECTIDE VACCINES
TITLE CF TRVENTION: DELIVERING POLYNOLECTIDE VACCINES
TITLE CF TRVENTION TRVENTION OF TRVENTION TRVENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2451 AACAACGAAAATAAGAACCCC......CATAACAAAA 2482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2533 ATAACAATAATAAAGAGTCATACCGGTCATTTTTCTTTACCAGCT 2582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2583 AATGCTTACCATAGAAGAAGTAACAGCTCTGTAACCAATAAT...... 2624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 AsnGlyGluGluAspArgProValGlyGlyGlyGluGlyHisGlnProAl 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 rgGlyGlnAlaArgArgLeuAlaProAsnPheArgTrpAlaIlePro... 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 ........ AsnArgGlnMetAsnAspGlyLeuGlyGlyAspGlyAspAs 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-155-888-1
                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-323-433A-3 from: 1 to: 3455
alignment_scores:
Quality: 79.00 tength: 92
Quality: 1.362 Gaps: 5
Percent Similarity: 63.043 Percent Identity: 26.087
                                                                                                                                                                                                                                  alignment_block:
US-09-327-750D-12 x US-09-323-433A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2653 AAATTCACTCTCCGCAACAATTA 2676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGRAT INFORMATION:
NAME: SEPORACE, DAVID
REDISTRATION WINBER: 24, 74
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 GluLeuGlnLeuArgAsnCysLeu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
; Sequence 1, Application US/08155888
; Settent No. 6066623
; GENERAL INPORMATION:
```

575	96 614	113 661										34
111::: 1 11 561CCCGAGGCCAGCCT5	80 etGlumetPhemetGluGluMetArgGluIleArgArgLysLeuArgGlu 9 ::::::::: 576CTACGCCGTCAAGGTACTCGCCCCACGGCAGCGGCCA 6	97 LeuGlnLeuArgAsnCysLeuArgIleLeuWetGlyGluLeuSerAsnH 1 ::: :::	113 sHisasphisHisaspolu 119 662 TGGACGTCATCAC 680	seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-387-942C-18	seq_documentation_block:	ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O. BOX 747 CITY: FALLS CHURCH STATE: VA	 CORRENT APPLICATION DATA PELLING DATE: 05-MX-1995 FILING DATE: 05-MX-1995 ATTOREX AGENTION: 435 ATTOREX AGENT HOTOMACHOON: RAME: MURPHY JR, GERALD M. REPERSUR/DOCKET NUMBER: 28,977 REPERSUR/DOCKET NUMBER: 1809-106P	TELEVAN: 703-205-8000	alignment_scores: 77.00 Length: 91 Quality: 77.00 Length: 91 Ratio: 1.711 Gaps: 4 Percent Similarity: 49.451 Percent Identity: 30.769	alignment_block: US-09-327-750b-12 x US-08-387-942C-18	Align seg 1/1 to: US-08-387-942C-18 from: 1 to: 1155	18 GlyGluGluAspArgProValGlyGlyGlyGluGlyHisGlnProAlaGl :

121 51 135	64 179 78	229 91 279	•				20	33	49	66	
72 GGCGATCGACGCCCCCACGGGGGGGGGGGCGCCCTCTACCTGCCGG 34 yAsnAsnAsnAsnAsnAsnHisAsnHisAsnHisAsnHisArgArgC 122 CCGCCAATATG	51 lyGlnAlaArgArgLeuAlaProAsnPheArgTrpAlalle	180 GAGCAACGTCCATATCGTCGGGGGGATGGGGGAGACGGTGATCAAGA 78 PASPWECGLUMETPHEMEGGLUGLUMETATGGLUILBA 130 TGGTCGACGCAGAACGTCACCGGCATGGTGGTGGCGTTGGCCTAC	91 rdArdLysLeuArgGluLeuGln 98 	seq_documentation_block: ;Patent No. 521881 ;Patent No. 521881 ;TITLE OF INVENTION: PSEUDORABIES DIAGNOSIS PROBES ;TITLE OF INVENTION: PSEUDORABIES DIAGNOSIS PROBES ; UNREEN PEPLICATION DATA: ;CURRENT APPLICATION NUMBER: 13-JUN-1990 ;FILING DATE: ;SEQ ID NO.2: ;SEQ ID NO.2: ;LENGTH: 2721 5215881-2	alignment_scores: 77.00 Length: 83 Ratio: 1.510 Gaps: 4 Percent Similarity: 61.446 Percent Identity: 27.711	alignment_block: US-09-327-750D-12 x 5215881-2 Align seg 1/1 to: 5215881-2 from: 1 to: 2721	5 HisGircipasnGluGluMetGluGlnProleuGlmAsnGlyGluGl :::: ::::	20 uAspA; yProValGlyGlyGlyGluGlyRis	33 ladly**. NonasnAsnAsnAsnHisAsnHisAsnHisAsnHisHishI ::::::::::::::::::::::::::::::::::::	49 gArgGlyGlnAlaArgArgLeuAlaProAsnPheArgTrpAlalleProA	66 snargClnMetasnaspGlyLeuGlyGlyAspGlyAspAspMetGlu 81

Page 1

Tue Mar 12 09:01:16 2002

```
23
112
34
34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a purified polypeptide capable of binding neurorophin receptor (p75-MR). The invention is useful for binding and modulating the activity of p75NR. The invention is useful for MGF-indeuced soppicals, which plays an important role in neurogenetic diseases. The peptide of the invention and p75MR are useful for inhibiting NF-kappab activation in a cell or a subject, for inducting espace 2 and espaces a certivity to cleave poly (ADP-inbose) polymerase and fragment nuclear DNA in a cell by co-expression of (1) and p75-MR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New p75-neurotrophin receptor-associated cell death executor (NADE) and
the gene encoding NADE, useful for meditating the activity of p75NTR
and for detecting neurodegenerative diseases
141.92 7
157.43 1
146.40 4
108.36 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 lyAsnAsnAsnAsnAsnAsnHisAsnHisAsnHisAshHisArgArg 50
/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH02898 + 84.50
/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA70218 + 81.00
/SIDS2/gcgdata/geneseq-geneseqn/NA2000.DAT:AAA70218 + 83.50
/SIDS2/gcgdata/geneseq-geneseqn/NA2000.DAT:AAA70218 + 83.50
/SIDS2/gcgdata/geneseq-geneseqn/NA2000.DAT:AAA71610 - 83.50
                                                                                seg_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF23528
                                                                                                                                                                                                                                  Neurotrophin receptor; p75-WWR; WGF-induced apoptosis; neurogenetic disease; NF-kappaB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 700 BP; 177 A; 188 C; 203 G; 132 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAF23528 from: 1 to: 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Fig 1; 134pp; English.
                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                      (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                 07-JUN-2000; 2000WO-US15621.
                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1999; 99US-0327750.
                                                                                                                         DNA; 700
                                                                                                                                                                                  22-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-327-750D-12 x AAF23528
                                                                                                            seq_documentation_block:

XX
AAF25528 stendard; DNN
XX
AAF25528 stendard; DNN
DE XX
XX
MOUSE NADE DNN
XX
MUS SP.
XX
XX
MUS SP.
XX
XX
MUS SP.
XX
XX
MUS SP.
XX
MUS SP.
XX
MUS SP.
XX
XX
MUS SP.
XX
MUS 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-061707/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
     OM of: US-09-327-750D-12 to: N_Geneseq_1101:* out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                   Search information block:
Oury: US-09-327-7500-12
Ouery: US-09-327-7500-12
Ouery: US-09-327-7500-12
Outabase sequences: 930621
Database length: 42665219
Search time (sec): 335-560000
                                 Date: Mar 11, 2002 3:42
```

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC01005

617 TATGCCT 623

```
Sequences AAF21614 - AAF2031 represent DNA sequences encoding human propreted with breast and overlan depresent sequences are associated with breast and overlan cancer. Included in the invention are sequences AAF22032. AAF22040 and AAF59129 withof are used in the invention and characterisation of the DNA and protein sequences of the invention. The breast and overlan cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; antidacterial antiinflammatory antiulicer; vulnerary; anticonvulsant antibacterial antiinflammatory, antiulicer; vulnerary; anticonvulsant antibacterial, antiinflammatory, antiulicer; vulnerary; anticonvulsant antibacterial, and protein sequences are used in the disposals of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteinties and increasts and equiness are used in the disposals, percention and treatment of immune disorders e.g. Addison's disease, callergies, autoinmune hemolytic aneant, autoinmune thyotoditis, callerses amblitus, croh's disease, multiple scherosis, rheumatoid athaltis and increative collisis; candiovascular disorders such as myocardial isochemnas; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and infectious diseases such as
                                                                                          New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 917 BP; 228 A; 203 C; 270 G; 211 T; 5 other;
                                                                                                                                                                                                                                        Claim 1; Page 581-582; 1299pp; English.
              WPI; 2000-611515/58.
P-PSDB; AAB58845.
```

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

Human secreted protein 5' EST, SEQ ID NO: 1003.

Dumas Milne Edwards J, Duclert A, Giordano J;

```
306 CAGGAAAACGAAGAAGGAGCAGCCTATGCAGAATGGAGAAGAAGACG 355
                                                                                                                                                                                            6 GlnGluAsnGluGluMetGluGlnProLeuGlnAsnGlyGluGluAspAr 22
                                                                                                                                                  22 gProvalGlyGlyGlyGluGlyHisGlnProAlaGlyAsnAsnAsnAsnA 39
alignment_scores:
Quality: 550.50
Guality: 5.193
Percent Similarity: 89.076
Percent Identity: 84.874
                                                                                   Align seg 1/1 to: AAF21748 from: 1 to: 917
                                                    alignment_block:
US-09-327-750D-12 x AAF21748
                                                                                                                                                                                                                                                                                                                                                                                                                 uMetPro 124
```

```
The present sequence is one of a large number of 5' EST9 derived from manks encoding secreted proteins. An ORP has been identified within the sequence. The 5' EST9 were prepared from total human RNAs or polyA+ RNAs dequence. The 5' EST9 were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences subsuly correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo off primed onby libraries. Such EST9 are not mRNAs and even in those cases where longer conk sequences have been obtained, the full 5' TRY is rarely included.'S EST9 are derived from obtained, the full 5' TRY is rarely included.'S EST9 are derived from burshs with intext? sends and can therefore be used to obtain full length encounted the second off the constant of the cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 ATGGCAAATATTCACCAGGAAAACGAAGAGATGGAGCAGCCTATGCAGAA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetalaAsnValHisGlnGluAsnGluGluMetGluGlnProLeuGlnAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 532 BP; 151 A; 121 C; 163 G; 91 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID 1003; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAC01005 from: 1 to: 532
alignment_block:
US-09-327-750D-12 x AAC01005
```

17 nGlyGluGluAspArgProValGlyGlyGlyGluGlyH1sGlnProAlaG 34

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT;AAH13750

```
The present invention describes primer sets for synthesising 5602 (cfull-inenth combas defined in the specification. Where a primer set (full-inenth combas defined in the specification. Where a primer set (cfull-inenth compasse) and oliqoped-of primer and an oliqonuclectide complementary of the complementary strand of a polynuclectide which comprises one of the 5602 nuclectide compless at least 15 nuclectides. On the complementary strand of a polynuclectide which compless as 3-end sequence complementary to the complementary strand of a polynuclectide which compless a 3-end sequence complementary to the complementary strand of a polynuclectide which comprises a 5-end sequence. Where the complementary of the specification. The primer sets can be used in antisease threapy and the 5-end sequence(3)* end sequence is selected from those defined in the specification. The primers acts useful for synthesising polynuclectides comprises the primers are also useful for synthesising polynuclectides comprises the primers are also useful for synthesising polynuclectides complementary full-length cDNAs. The primers also useful for synthesising polynuclectides complement and performantly of the full-length cDNAs. The primers also useful for AM13531 to AM13671 to
                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length ODNAs
                                                                                      Ota I, Isogai I, Nishikawa I, Hayashi K, Saito K, Yamamoto J;
Ishii S, Sugiyama I, Wakamatsu A, Nagai K, Otsuki I;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 352; 2537pp + CD ROM; English.
                  (HELI-) HELIX RES INST.
                                                                                                                                                                                                   WPI; 2001-318749/34.
```

Sequence 865 BP; 239 A; 177 C; 224 G; 221 T; 4 other;

```
336 AT.....ATCAGGGGGG 349
                                                                                                                                                                                                                                                                                          3 AsnValHisGlnGluAsnGluGluMetGluGln...ProLeuGlnAsnGl 18
                                                                                                                                                                                                                                       35 snAsnAsnAsnAsnHisAsnHisAsnHisAsnHisHisArgGly 51
                                                                                                                                                                                                                                                                                                                                              68 nMetAsnAspGlyLeuGlyGlyAspGlyAspMetGluMetPheMetG 85
alignment_scores:
Quality: 264.50 Length: 123
Ratio: 3.112 Gaps: 4
Percent Similarity: 69.106 Percent Identity: 47.967
                                                                                                       Align seg 1/1 to: AAH03517 from: 1 to: 865
                                                                alignment_block:
US-09-327-750D-12 x AAH03517
```

```
The present invention describes primer sets for synthesising 5602

(1011-length Combus defined in the specification. Where a primer set

(2011-length Combus defined in the specification. Where a primer set

(2012) an oliquo-dry primer and an oliquouclocide complementary

(2012) the complementary strand of a polynusleotide which comprises one of

(2012) the 5602 mucleotide sequences defined in the specification, where the

(2013) the specification where the complementary strand of a polynusleotides; or (b) a combination

(2014) complementary strand of a polynusleotide with comprises a 5'-end

(2014) sequence and an oliquoucleotide comprising a sequence complementary to a

(2014) sequence and an oliquoucleotide comprising a sequence complementary to a

(2014) sequence and an oliquoucleotide comprising a sequence complementary to a

(2014) sequence and sequence as 1 sequence complementary to a

(2014) sequence and sequence as 1 sequence where the

(2014) sequence and sequence as 1 sequence where the

(2014) sequence and sequence as 1 sequence where the

(2014) sequence and sequence as 1 sequence where the

(2014) sequence and sequence as 1 sequence where the

(2015) sequence and sequence as 1 sequence where the

(2015) sequence and sequence as 1 sequence where the

(2016) sequence and sequence as 1 sequence where the

(2016) sequence and sequence as 1 sequence as 1 sequence and a s
                                                                                                                                                                                                                                                 Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length conks defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length conks.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID 10656; 2537pp + CD ROM; English.
                                                                                                                                                                                           Human cDNA sequence SEQ ID NO:10656.
```

```
312 GAGGAAAT.....CGTAGG 325
         seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH45143
                           alignment_block:
US-09-327-750D-12 x AAH45143
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA87080 to AAA87656 represent nucleic acid sequences (NI) encoding a acariongenesis biomarkers. The arctinogenesis biomarkers are induced by treating rat hepatocytes with phenobarbitol. The nucleic acids are acids are acid for identifying carcinogenic compounds. The nucleic acid molecules can be used to derive probes and/or primers for detecting or inducing carcinogenesis, respectively.
                                                                                                                                                                                   Rat; phenobarbitol; carcinogenesis marker; carcinogenesis; detection; identification; carcinogenic; probe; primer; ds.
                                                                                                                                                              Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:71.
                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding a carcinogenic biomarker, induced by membrabilo ireament of rat hepatocytes, useful for identifying carcinogeatic compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 TATATGCGCTTCCAAACTCCTGAACCTGACAACCATTATGAC..... 594
                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA87147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality: 193.00 Length: 35
Ratio: 5.514 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 187 BP; 39 A; 48 C; 40 G; 60 T; 0 other;
                                                                                                                                                                                                                                                                                                                                               Bunch RT, Curtis SW, Rodi CP, Morris DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAA87147 from: 1 to: 187
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 73; 240pp; English.
                                                                                    seq_documentation_block:
ID AAA87147 standard; DNA; 187 BP.
                                                                                                                                                                                                                                                                                28-JAN-2000; 2000WO-US00503.
                  99US-0118078.
                                                                                                                                       08-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-327-750D-12 x AAA87147
                                                                                                                                                                                                                                                                                                                          (SEAR ) SEARLE & CO G D.
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-505977/45.
                                                                                                                                                                                                                   Rattus norvegicus.
                                                                                                                                                                                                                                       W0200044902-A2.
                                                                                                                                                                                                                                                                                                    29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 etPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 TGCCT 106
                                                                                                                                                                                                                                                           03-AUG-2000.
                                                                                                                   AAA87147;
```

```
Human, brain expressed X-linked protein; cytostatic; auditory; nootropic; Hems; dysemiryoplasis; heedlitary disease; cancer; tumour; deafiness; X-chromosome-binding mental retardation; lissencephalous disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the coding sequence for a human brain-expressed X-linked protein (BRSA). Has and its coding sequence are useful in the diagnosis and treatment of dysembryoplasis, hereditary diseases, cancer, tumours, deafness, X-chromosome-binding mental retradition and ilssencephalous disease. Has the useful for screening mimics, agonists, or inhibitors, and in peptide fingerprinting identification. Has coding sequence can be used as primers or probes, or in producing gene chips or microarrays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated human brain-expressed X-linked polypeptide used to diagnose and treet of dysembrophasia, hereditary diseases, cancer, tumor, deafless and X-chromosome-binding mental retardation
Human brain expressed X-linked protein, hBex, coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :||i|||
262 AGGGGAGCCCTTGGCCCTCCCTTTGGATGCTGGTGAATACTGTGCCTA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetAlaAsnValHisGlnGluAsnGluGluMetGluGlnProLeuGlnAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 nGlyGluGlu. . AspArgProValGlyGlyGlyGluGlyHisGlnProA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 laGlyAsnAsnAsnAsnAsnAsnHisAsnHisAsnHisAsnHisArg 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 792 BP; 214 A; 172 C; 219 G; 187 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAH45143 from: 1 to: 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.
```

us-09-327-750d-12.rng

Tue Mar 12 09:01:16 2002

AAF59611 standard; cDNA; 898 BP.

ID NO:76.

Human cell cycle and proliferation protein CCYPR-22 cDNA, SEQ

24-APR-2001 (first entry)

AAF59611;

cell cycle and proliferation protein; CCYPR; human; agonist; antagonist; gene therapy; detection; gene therapy; transgenic animal disease model; immune disorder; reassgenic animal disease model; immune disorder; cell elevelopmental disorder; cell signaling disorder; elevenour; anamala; epilepsy; arterioscierosis; sathma; allergy; diabetes mellitus; menstrual cycle disorder; bacterial infection; ss.

```
The invention relates to human nucleic acids (AAIS7789-AAI61369) and the encoded polypeptides (AAAI86213) with noctropic. Immunosuppressant and cytostatic acitylity. The polynucleotides are useful in one therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, ench as the peripheral nervous statistics and shy-brager Syndrome. Other uses include the lateral sclerosis, and shy-brager Syndrome. Other uses include the activity of the activity of selementatic activity, haemostatic and thromboty creativity, cancer disgnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leavemiss and this orders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification.
                                                                     Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 CTAGAGGAAAC.....CGT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385 AGGCGGTTCCGCGTTAGGCAGCCCATCCTGCAGTAAAAAGATGGGACATAAT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 PORTER PROPERTY GLINKELASIA REPOLITION 76
435 GCATAGGCTTGGAGAGCCAAGGAAGAACAAA (A 171)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 LysLeuArgGluLeuGlnLeuArgAsnCysLeuArgIleLeuMetGlyGl 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 spGlyAspAspMetGluMetPheMetGluGluMetArgGluIleArgArg 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AsnvalHisGlnGluAsn......GluGluMetGluGlnProLeuGl 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 nAsnGlyGluGlu... AspArgProValGlyGlyGlyGluGlyHisGlnP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 roAlaGlyAsnAsnAsnAsnAsnAsnAsnH19AsnH1sAsnH1sH1s 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 ArgArgGlyGlnAlaArgArgLeuAlaProAsnPheArgTrpAlaIle.. 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF59611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 862 BP; 235 A; 183 C; 238 G; 206 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality: 171.50 Length: 132
Ratio: 2.287 Gaps: 6
Percent Similarity: 56.818 Percent Identity: 36.364
                                                                                                                                                  Claim 1; SEQ ID NO 784; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AA158581 from: 1 to: 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-327-750D-12 x AAI58581
WPI; 2001-442253/47.
P-PSDB; AAM39425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
```

Hillman Ji, Lal P, Tang YT, Yue H, Au-Young J, Bandman O; Azimzai Y, Yang J, Lu DAM, Baughn MR, Patterson C, Shah P;

WPI; 2001-112727/12. P-PSDB; AAB60474.

21-JUL-2000; 2000WO-US19948. 21-JUL-1999; 99US-0145075, 08-SEP-1999; 99US-0153129, 10-NOV-1999; 99US-0164647. (INCY-) INCYTE GENOMICS INC.

WO200107471-A2. Homo sapiens.

01-FEB-2001.

```
Sequences AAF5950-AAF59643 represent cDNAs encoding 54 human cell cycle and proliferation proteins (CCPPA, AAB60543-AAB6056.
CCTPR and agonists of CCPPR are used to treat diseases or conditions associated with decreased expression of functional CCPPR, while CCPPR antagonists are used to treat diseases or conditions associated with overexpression of functional CCPPR. Monoclonal or polyclonal antibodies to CCPPR may be used in enzyme-linked immunosochent assays (ELISA) or radoimmunosasys to detect CCPPR CCPPR in an expection of functional CCPPR, and in drug screening method to compounds ery antibodies of that specifically bindodes oldered the activity of CCPPR CCPPR compounds that modulate the activity of CCPPR CCPPR CCPPR compounds that modulate the activity of CCPPR CCPPR CCPPR content of the compounds that modulate the activity of CCPPR CCPPR CCPPR content of the compounds the condition of the activity of CCPPR CCPPR CCPPR content of the compounds the condition of the activity of CCPPR CCPPR CCPPR CCPPR content of the compounds the condition of the compounds to the compound of the compounds to the compound of the compounds the condition of the compounds to the compound of the compounds to the compound of the compounds to the compound of the compound of the compound the compound the compound of the compound of the compound of the compound the the compound of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cell cycle and proliferation proteins and polynucleotides are
used to treat, diagnose and prevent immune, developmental and cell
signaling disorders and cell proliferative disorders including cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 898 BP; 250 A; 186 C; 251 G; 211 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171.50 Length: 132
2.287 Gaps: 6
56.818 Percent Identity: 36.364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 181-182; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
Quality:
Ratio:
Percent Similarity:
```

```
obtained, the full 5' UTR is rarely included. 5' ESTs are derived from whise with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs 3' ESTs are also used in dispinctio, forensic, gene thereby and chromosome mapping procedures. They are used to obtain vectors.
                    8888888
```

Seguence 662 BP; 177 A; 144 C; 192 G; 137 T; 12 other;

				31 12
126	35.714			o tong of p
Length: Gaps:	Percent Identity: 35.714		to: 662	at touchand tout and tout a
	Percent	:	from: 1	ē
162.50	54.762	AAC03880	AAC03880	-01
cores: Quality: Ratio:	milarity:	10ck: 750D-12 x	1/1 to:	
alignment_scores: Quality: 162.50 Ratio: 2.355	Percent S1	alignment_block: US-09-327-750D-12 x AAC03880	Align seg 1/1 to: AAC03880 from: 1 to: 662	,

16 nAsnGlyGluGlu...AspArgProValGlyGlyGlyGlyGlyHisGlnP 32 ::::|||||||

65 oAsnArgGlnMetAsnAspGlyLeuGlyGlyAspGlyAspAspMetGluM 82

```
house mouse.

Kan manala: Butheria: Rodentia: Craniata; Vertebrata; Euteleostomi; Eukaryock; Mercan; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryock; Mercan; Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 700)

Musi, J. Hachiya; T. Shoij-Heshinos. Kimura, M.; Nadarop, D.; Suvanto, P.; Hansoka, T.; Lily, T. Itie, S.; Gemen, L.A. and Sato, T.A. NNDE; a p75NTR-associated cell death executor, is involved.

J. Biol. Chem. 275 (23), 17566-17570 (2000)

E. Classes 1 to 700;
E. Classes 1 to 700;
E. Muxai, J.; Hachiya; T.; Hoshino, S.; Kimura, M.; Nadano, D.; Suvanto, P.; Rimack, T.; Lily, T.; Lile, S. and Sato, T.

Direct Submission

I. Submitted (17-SEP-1999) otolaryngology/Pathology, Columbia

Interest Submission

I. Submitted (17-SEP-1999) otolaryngology/Pathology, Columbia

I. Too

I. Submitted (17-SEP-1999) otolaryngology/Pathology, Columbia

I. Too

I. Submitted (17-SEP-1999)

I. Too

I. Too
10807 | AB004899 Pseudomonas ae. 14499 | AB016876 Arabidopsis th. 76072 | AL355927 Neurospora cra. 158807 | AC011771 Homo saptens v. 2794 | X54157 S.cerevisiae FPS1
                                                                                                                                                                                               seq_documentation_block: 700 bp mRNA ROD (11-JUN-2000) LOCUS AF187066 700 bp mRNA ROD (11-JUN-2000) REPRIVATION MUS musoculus p75NTR-associated cell death executor (Nade) mRNA ACCESSION AF187066.1 G1:8452897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouslicy: 688.00 Length: 124
Ratio: 5.548 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.387
33.27
138.96
291.18
612.42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AF187066 from: 1 to: 700
   134.31
123.16
117.39
111.60
100.00
100.00
99.00
99.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-327-750D-12 x AF187066
                                                                                                                                                   seq_name: gb_ro:AF187066
gb_ba:AE004899
gb_pl:AB016876
gb_pl:NCB1D1
gb_htg:AC011771
gb_pl:SCFPS1G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Documentation | Documentatio
                                                                                                                                                                    About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
OM of: US-09-327-750D-12 to: GenEmbl:* out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search information block:
Overy: US-09-322-7500-12
Overy: US-09-322-7500-12
Detabase: Genimm: Detabase sequences: 1472140
Detabase Bergin: -3144637
Search Lime (sec): 4557.230000
                                           Date: Mar 11, 2002 3:33 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score_list:
Sequence
Sequence
Sequence
Sequence
Sp_cr.RF07066
Sp_cr.RF07065
Sp_cr.RE0001390
Sp_cr.RE0001390
Sp_cr.RE0001390
Sp_cr.RE187064
Sp_cr.RE187064
Sp_cr.RE187064
Sp_cr.RE187064
Sp_cr.RE187064
Sp_cr.RE20189
Sp_cr.RE2018189
Sp_cr.RE201
```

```
alignment_block:
US-09-327-750D-12 x BC003190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                             REFERENCE
AUTHORS
TITLE
JOURNAL
             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REMARK
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
/organism-"Rattus norvegicus"
/dsrain-"Sprague-Dawley
/db_cree-"Sprague-Dawley
/db_cree-"Sprague-Dawley
/dp_cree-"Sprague-Dawley
/gene-"Bade
/gene-"Bade
/gene-"Involved in the common neurotrophin receptor
pySngs-medated signal transduction; NADE"
/codon_start-1
/codon_tart-1
/product-"SySngs-associated cell death executor"
/product-"SySngs-associated cell death executor
/product-"SySngs-asso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block: 193 bp mRNA pRI 112-JUL-2001 LOCUS SCOOLS SCOOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AF187065 from: 1 to: 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 sHisAspGluPheCysteuMetPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 TCACGATGAATTCTGCCTTATGCCT 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-327-750D-12 x AF187065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_pr:BC003190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                              CDS
```

```
CREARIENT HORD SABLERS

REFERENCE

REMARYOR IN THE STREAM OF THE STREAM OF CHARLES, Vertebrats, Eutheled Fundamiles Eutheled To 731)

REFERENCE

RICHARGE OF THE STREAM OF 731

TITLES

DITCHARGE OF SUBMISSION

REMARKED TO THE STREAM OF THE S
```

```
Manmalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 421)
Pahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L. and
Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of 20 or greater Amplicon size was estimated by agarose gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 opnotes 1. (21 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1. (22 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Template: 50-200 ng genomic DNA Primer: each 20 pmoles each 30 du du Pres: each 80 uM rag Polymerase: 0.25 units (Qlagen HotStar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Commercially supplied Qiagen HotStar buffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Freking BA
USDA, ARS, US Weat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 427 Senter
Fax: 402 762 4173
Email: Frekingemail:marc.usda.gov
Primer A: GCAAATGGGTAAACTFACT
STS Size: 500
PCR PZOÉLIE: ACCAGGAAATAGAGG
PCR PZOÉLIE: ACCAGGAAATAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 411.00 Length: 77 Retio: 5.338 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 96.104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: G72708 from: 1 to: 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Horstart: 95 degrees for 15 minutes
Denature: 95 degrees for 30 seconds
Anneal: 56 degrees
Extension: 68 degrees for 2 minutes
Cycles: 32 to 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 g 102 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-327-750D-12 x G72708/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <1. .>421
101 c
                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protoco]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STS
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foodon_start=1

/product=197878-associated cell death executor*

/product=197878-assoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pig.
19 scorofa
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS (772708 772708 772708 772708 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 772701 77270
                                                                                                                                                                                                                                                                                          312. 647
gree-Nable in the common neurotrophin receptor
p75NTR-mediated signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          412 GAAAT.....CGACGG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 AsnCysLeuArgIleLeuWetGlyGluLeuSerAsnHisHisAspHisHi 117 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 etGluGluMetArgGluIleArgArgLysLeuArgGluLeuGlnLeuArg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetalaAsnValHisGlnGluAsnGluGluMetGluGlnProLeuGlnAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 lyAsnAsnAsnAsnAsnHisAsnHisAsnHisAsnHisAsnHisArgArg 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 g 234 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AF187064 from: 1 to: 891
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="NADE"
312, .647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G72708
G72708.1 GI:15146738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-327-750D-12 x AF187064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_sts:G72708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
```

```
alignment_block:
US-09-327-750D-12 x AK000959
                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKO00959.1 GI:7021945
AKO00959.1 GI:7021945
Oligo capping; fis (full insert sequence).
Homo saptens embryo, 10 vecks whole embryo, mainly head cDNA to mRAA, clone_lib HEBABA! clone:HEBABA100458.
ISM Homo saptens
EUKATYOCIA; HETAZOCA: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominides; Homo.
El (sites)
I (sites)
I (sites)
A Manualia; Eutheria; Primates; Catarrhin; Hominides; Homo.
The A Manualia; Fight Sites (Sites)
A Mishikwar T., Nagah, K., Sugano, S., Takabashi-Fullia,, Hara, H., Tanase T., Nomura Y., Toglya, S., Komai, F., Hara, R., Takeuchi, K., Anta, M. Nabekura, T., Ishi, S., Kawai, Y., Saito, K., Yamamoto, J., Hakamatau, A., Makamuta, Y., Nagahari, K., Masuho, Y. and Oshima, A.
NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKO00959 .... 1229 bp mRNA PRI 027-FEB-2000 Homo sapiens CDNA FLJ10097 fis, clone HEMBAL002458, weakly similar to Oyatan Granulosa CELL 13.0 KD PROFEIN HGR74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             19561 AAAGGGGTTGGGCTCCACCTGCCCGGGTTTTGGAGAGGATGTGCCCAA 19610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19506 GAAT.....GAAGCCCCCGCTTTAGGAGGTGGTGAATACCAGGAGCCTG 19549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19550 GAGGAAAT.....GTT 19560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 GlnLeuArgAsnCysLeuArgIleLeuWetGlyGluLeuSerAsnHisH1 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 ArgGlyGlnAlaArgArgLeuAlaProAsnPheArgTrpAlaIleProAs 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 nAsnGlyGluGluAspArgProValGlyGlyGlyGluGlyHisGlnProA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 laGlyAsnAsnAsnAsnAsnAsnAsnHisAsnHisAsnHisHisArg 49
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetalaAsnValHisGlnGluAsnGluGluMetGluGln...ProLeuGl 16
                                                                                                                                                                                                                           repeat_region 38747. 38839.

fonce=wildTiR element fragment*
repeat_region 39949. 39032

repeat_region 39965. 39076

BASE COUNT 14260 9135 C 9227 9 12956 t
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: HSV351F8 from: 1 to: 45678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19758 TGATCATCATGAGTTTTGCCTTATGCCT 19788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 sAspHisHisAspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-327-750D-12 x HSV351F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS AK000959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_pr:AK000959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
```

```
L Unpublished (2000)

E 16241. and Cutakk,T.

S ISOGALT. and CLEER 2000) to the DDBJ/EMBL/GenBank databases. Takao
Direct Submitsed (16-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takao
Submitted (16-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takao
Submitted (16-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takao
Submitted (16-FEB-2000) to the DDBJ/EMBL/GenBank GenBank
Kisarzau, Chibe 292-0612, Japan (E-mail:genomicsaprotory; 1532-3 Yana,
Kisarzau, Chibe 292-0612, Japan (E-mail:genomicsaprotory) for Japan
FED Naman CDNA seperated Dy Ministry of
International Trade and Industry of Vapan; CDNA full Insert
Construction, 5' - 6' 3'-end one pass sequencing and clone selection:
Hellx Research Institute (Supported by Japan Key Technology Center
etc.) and Departement of Virology, Institute of Medical Science,
University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /orgalism-thomo sapiens'
/orgalism-thomo sapiens'
/orgalism-thomo sapiens'
/orgalism-thomo sapiens'
/clone_lib-"HEMBA100458'
/clone_lib-"HEMBA100458'
/dev_stope-"whole embryo, mainly head'
/dev_stope-"whole embryo, mainly head'
/note-"loning vector: pWEB185F13'
/note-"unnamed protein product'
/codon_start-1
/protein_id-"sapi443.1'
/protein_id-"sapi43.1'
/protein_id-"sapi44.1'
/protein_id-"sapi44.1'
/protein_id-"sapi44.1'
/protein_id-"sapi44.1'
/protein_id-"sapi44.1'
/protein_id-"sapi44.1'
/protein_id-"sapi44.1'
/protein_id-"sapi44.1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 AT.....ATCAGGGGG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 luGluMetArgGluIleArgArgLysLeuArgGluLeuGlnLeuArgAsn 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 AGAAGAATCCCGCCATTTGGGAGGGGTGAAGGCCAGAAGGCTGGAGGAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 GGCAGATGATGGAAATCAAGAGAAAGACTAGGGAACAGCAGATGAGGCAC 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 CysLeuArgileLeuMetGlyGluLeuSerAsnHisHisAspHisHisAs 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 yGluGluAspArgProValGlyGlyGlyGluGlyHisGlnProAlaGlyA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 snAsnAsnAsnAsnHisAsnHisAsnHisAsnHisHisArgArgGly 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 nMetAsnAspGlyLeuGlyGlyAspGlyAspAspMetGluMetPheMetG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores;
Quality: 264.50 Length: 123
Ratio: 3.112 Gaps: 4
Percent Similarity: 69.106 Percent identity: 47.967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AK000959 from: 1 to: 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .1229
```

repeat_region

repeat_region

/note="MIR repeat: matches 109. 217 of consensus" /note="LIME2 repeat: matches 58256022 of consensus" /note="LIME2 repeat: matches 58256022 of consensus" /note="Aluga repeat: matches 1313 of consensus" /note="Aluga repeat: matches 55835825 of consensus" /note="Aluga repeat: matches 1311 of consensus" /note="Aluga repeat: matches 1311 of consensus" /note="Aluga repeat: matches 53045591 of consensus" /note="Aluga repeat: matches 53045591 of consensus"	7.01. 1.1. And Tepeat: matches 55586162 of consensus. 7.02413413	1357. 1377 12. 1329 12. 1329 13. 1357 1. 1357 1. 1357 1. 135 1. 1	/note-*AluSx repeat: matches 24. 312 of consensus* 1066. 10363 /note-*AluSx repeat: matches 1. 291 of consensus* 1042. 16641 /note-*AluSx repeat: matches 136. 295 of consensus* 10671. 16953 /note-*AluSx repeat: matches 1. 284 of consensus* 17164. 17280 /note-*LIP repeat: matches 4499. 4619 of consensus*
repeat_region repeat_region repeat_region repeat_region	region	repeat_region	repeat_region repeat_region repeat_region repeat_region

```
17726. 17377
17704. 17377
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17364.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17363.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
17704. 17704.
1770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
Quality: 264.50
Guality: 3.112
Percent Similarity: 69.106
Percent Identity: 47.967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: HS635G19 from: 1 to: 69648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-327-750D-12 x HS635G19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                repeat_region
                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                             repeat_region
                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
```

```
/note-'MER31B repeat: matches 2. .162 of consensus' 3156. 31094 force-'MIR repeat: matches 218. .256 of consensus' 31728. 31791 force-'MIR repeat: matches 4 mer tgtg 76 conserved' 31858. 31952 force-'MIR repeat: matches 48. .153 of consensus' complement(3447. .33589) force-'match: STS: Em:H55731' 33543. .33533. /3764-'MIR repeat: matches 84. .165 of consensus' /note-'MIR repeat: matches 84. .165 of consensus' /note-'MIR repeat: matches 1. .185 of consensus' /note-'MIR repeat: matches 1. .185 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 yLeuGlyGlyAspGlyAspAspMetGluMetPheMetGluGluMetArgG 89
                                                                                                                                                                                                                                                                                                                                                                                                Alignment_scores: Length: 67 (Quality: 240.50 Gaps: 2 Ratio: 4.076 Gaps: 2 Percent Similarity: 88.060 Percent Identity: 77.612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: HS714B7 from: 1 to: 98274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Denaturation:
Annealing:
Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-327-750D-12 x HS714B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS
G32594
ACCESSION
G32594
VRENION
G32594.1 GI:24:
KEYWORDS
STGS
SURCE
ONGANISM Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_sts:G35294
                                       repeat_region
                                                                                              repeat_region
                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /20.25 . 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97 / 20.97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="%18.repeat: matches 82. .262 of consensus"
/note="%18. 20741
/note=".20765". .2074
/note=".20765". .21074 repeat: matches 5970. .6224 of consensus"
/note="%18.repeat: matches 1. .303 of consensus"
/1085. .21207
                                                                                                                           | 16897. 17005
| 16897. 17005
| 17618. 17700
| 17618. 17700
| 17618. 17700
| 1762-*MIR repeat: matches 9. 118 of consensus*
| 1778. 17912
| 1762-*MIR repeat: matches 73. 245 of consensus*
| 18677. 18671
| 18677. 18671
| 1872. 19230
| 1972. 19230
| 1972. 19230
| 1972. 19230
| 1972. 19230
| 1972. 19730
| 1972. 19730
| 1972. 19730
| 1973. 19730
| 1973. 19730
| 1973. 19730
| 1973. 19730
| 1973. 19730
| 1973. 19730
| 1973. 19730
| 1973. 19730
| 1973. 19730
| 1973. 19730
| 1973. 19730
| 1973. 19730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ter LINZ repeat: matches 1776. .1898 of consensus" ter LIND repeat: marche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="12 repeat: matches 2330. 2519 of consensus" 25673. 2591 repeat: matches 4. 255 of consensus" 2679. 22798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 //Acte-12 repart: matches 2572. .2649 of consensus.
7040. .2707
//Acte-12 repart: matches 2489. .2500 of consensus.
72108. .27108. .27108. .27108. .27108. .27108. .27108. .27108. .27108. .27108. .27108. .27108. .27108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7/31/5. .4.44.1

// Anote="12 repeat: matches 2372. .2489 of consensus"

27651. .27945

// Anote="Allox repeat: matches 1. .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dotte="iJMD repeat: matches -6. .178 of consensus"
21392 .21471 repeat: matches 3. .86 of consensus"
22146. .22441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48/1. .24916
740=*MIR repeat: matches 102. .143 of consensus*
2378. .2555
/note=*LZ repeat: matches 2330. .2519 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ux repeat: matches 41. .304 of consensus"
7471
                                    R repeat: matches 102. .144 of consensus"
6184
                                                                            vollo. .lold4
//note="MRENE repeat: matches 3. .70 of consensus"
16897. .17005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28235. .28876
/note="L2 repe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21085. .2120
/note-"L1M2
21212. .2139
                  repeat_region
                                                                        repeat_region
                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
```

```
human.

Human.

Bukan sapiens

Bukaryota.

Hammalia: Butheria: Primates: Catarrhini: Hominidae; Homo.

Hosess 1 to 477)

Wyers.R.M.

Unpublished (1997)
                                                                                                                                             02-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 degrees C for 15 seconds
60 degrees C for 30 seconds
72 degrees C for 23 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial incubation: 95 degrees C for 10 minutes
                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Richard M. Myers
Stanford Human denome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 417729669
Ema: 117729669
Ema: 117729669
G35294 477 bp DNA STS
G35294 5035294 1 G1:2459462
F35294 1 G1:2459462
F35: STS sequence; primer; sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer A: AACATCTTTCCATGAAAGTTGATG
Primer B: CTTTTGGCATTCTTCTGCAA
STS size: 106
PCR Profile:
```

```
Hommon.

Elemon Sappiens

Az Oldoria Sappiens

Az Oldoria Sappiens

Az Oldoria Sappiens

Az Oldoria Sappiens

Elemon Sappiens
AF220189 828 bp mRNA PRI 04-MAY-2000 Homo sapiens uncharacterized hypothalamus protein HBEX2 mRNA, complete cds.
AF220189.1 GI:7689028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 laGlyAsnAsnAsnAsnAsnAsnHisAsnHisAsnHisHisHisHig 49
306 GAGGAANT COTAGG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 TAGGCTTGGAGAACCACAGGAAGGATGAGAA......403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 ......ProAsnArgGlnMetAsnAspGlyLeuGlyGlyAspG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 nGlydluGlu. .. AspArgProvalGlyGlyGlyGlyGluGlyHisGlnProA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 ArgGlyGlnAlaArgArgLeuAlaProAsnPheArgTrpAlaIle.... 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 lyaspaspMetGluMetPheMetGluGluMetArgGluIleArgArgLys 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
Quality: 191.00 Length: 131
Ratio: 2.513 Gaps: 5
Percent Similarity: 58.015 Percent Identity: 37.405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AF220189 from: 1 to: 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-327-750D-12 x AF220189
                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
             LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
```

```
452 CTGAGGAAAAGAATTAGATCATAGTCTGCGGGCAGTCAGCACTGAC.. 499
110 userhaniishishaphiishishapqluphactysLeuMetPro 124
500 .CCCCTACACATGACATCATGATAGTTTGCTTATGCC 541
```

```
Seq_documentation_block: 492 bp mENA
DEFINITION WESHOL: Soares mouse embryo MbELL: 5.415 Mus musculus CDNA
ACCESSION Weshold: 10 to PROFEED HORY (HUMAN); mRNA sequence.
11.0 KD PROFEED HORY (HUMAN); mRNA sequence.
12.0 KD PROFEED HORY (HUMAN); mRNA sequence.
13.0 KD PROFEED HORS (HUMAN); mRNA sequence.
13.0 KD PROFEED HORY (HUMAN); mRNA sequence.
13.0 KD PROFEED HORS (HUMAN); mRNA sequence.
14.0 KD PROFEED HORS (HUMAN); mRNA SECOUNC.
14.0 KD PROFEED HORS (HUMAN); mRN
   B1281721 UI-R-CTOS-Cav-f-.
BF168928 601775392F1 NOT_!
AA214909 mu76f05.r1 Strati
AI183075 ub53e07.r1 Soare:
AI157489 ue56e05.r1 Soare:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 124
Gaps: 0
Percent Identity: 98.387
5.8e-50
3.0e-49
4.0e-49
6.5e-49
1.2e-48
   628.00 1061.48
621.50 1048.73
618.00 1046.43
615.00 1042.69
611.00 1037.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality: 688.00
Ratio: 5.548
Percent Similarity: 100.000
                                                                                                                                                              seq_name: gb_est2:W46041
   gb_est2:BT281721
gb_est2:BF168928
gb_est1:AA214909
gb_est1:AI183075
gb_est1:AI183075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11gnment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Documentation | Documentation | Aconsection | MAGGAI mcRAIDO.: I Scares mouse | MAGGAI mcRAIDO.: I Scares mouse | MAGGAI mcRAIDO. I Sugano mous | MAGAISOTO mm76604.179 | Scares_mamm | MAGAISOTO mm76604.179 | Scares_mamm | MAGAII md71g01.: I Strategene | BE3487 me95406.17 | Scares_mamm | MAGAII md71g01.: I Scares mouse | MAGAIST me95406.1. Scares mouse | MAGAIST me95406.1. Scares mouse | MAGAIST me95406.1. Scares mouse | AACIST me95406.1. Scares mouse | AACIST me95406.1. Scares mouse | AACIST me95406.1. Scares mouse | MAGAIST me75406.1. Scares mouse | MAGAIST me75406.1. Scares mouse | MAGAIST me75407. I Scares mouse | MAGAIST me75407. I Scares mouse | MAGAIST me76407. I Scares mouse | MAGAIT me76407. I Sc
                                                                                                                                                                                   Command line parameters:
-WODE-frame-pD. model = .DEV-x1h
-WODE-frame-pD. model = .DEV-x1h
-WODE-frame-pD. model = .DEV-x1h
-DECEST -OFFW-fastap - SUFFEX-ret -GROPE-12.000 -GARPET-4.000
-GAPPET-9.000 -KODPCL-0.000 -KOAPPET-0.000 -GRAPP-4.500
-GAPEXT-0.000 -KAPPD-10.000 -KOAPPET-0.500 -FGAPP-6.000
-FGAPEXT-0.000 -KAPPD-10.000 -KOAPPET-0.500 -FGAPP-6.000
-FGAPEXT-0.000 -FARPO-10.000 -KOAPPET-0.500 -FGAPP-6.000
-FGAPEXT-0.000 -FARPO-1-10.000 -KOAPPET-0.500 -FRANS-human40.cdi
-LIST-4. -OMODELACAL -OMTH. SCORE-PCT -THR. ANAL-100 -THR. MIN-0
-ALIGN-15 - WODE-LOCAL -OMTPAT-PFS - WORN-ext -HEAPSIZE-500
-WINKLEN-0.000000000 -USER-US09327750.eCGN1.1_5654
-WCPD-6 -SCPD-3 -LANGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30
                                                                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
          out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10019

5080 0 1165.70

6080 0 1164.21

6080 0 1164.21

6080 0 1164.21

6080 0 1164.21

6080 0 1164.21

6080 0 1164.20

6080 0 1163.60

6090 0 1163.60

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6730 0 1163.25

6740 0 1163.25

6750 0 1163.25

6750 0 1063.25

6750 0 1063.25

6750 0 1063.25

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55

6750 0 1063.55
       EST: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search information block:
Ouery: UG-09-327-750D-12
Ouery length: 124
Detabase sequences: 11351937
Database length: 1077921985
Search time (sec): 4085.940000
       t0:
                                                               Date: Mar 11, 2002 2:16 PM
       OM Of: US-09-327-750D-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secure 1184:

Described (MI)

Described (MI)
```

Page 3

Tue Mar 12 09:01:17 2002

```
1 MetalaasnValHisGlnGluAsnGluGluMetGluGlnDroLeuGlnAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AA215070 from: 1 to: 557
                            117 sAspGluPheCysLeuMetPro 124
                                      S16 TGATGAATTCTGCCTTATGCCT 537
                                                                                                             AA215070
AA215070.1 GI:1814831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-327-750D-12 x AA215070
                                                          seq_name: gb_est1:AA215070
                                                                                                                                              musculus
                                                                                                                                    house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                   159 a
                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                             TITLE
JOURNAL
COMMENT
                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                     FEATURES
 266 CAAACAACAACAACAACCACAAACCATAACCACAACCACACACACAAGA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 etGluGluMetArgGluIleArgArgLysLeuArgGluLeuGlnLeuArg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 lyAsnAsnAsnAsnAsnHisAsnHisAsnHisAsnHisAsnHisHisArgArg 50
                                                                                                                                                                                                                                                                                            alignment_scores;

Quality: 688.00 Length: 124
Quality: 5.548 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.387
                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: BE334866 from: 1 to: 542
BE334866.1 GI:9208642
                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-327-750D-12 x BE334866
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                             source
                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                          REFERENCE
AUTHORS
TITLE
                                                                        JOURNAL
                                                                                                                                    FEATURES
```

```
Answinson Musical Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Solorognathi; Muridae; Musica; Marra, M.; Hillier, L., Allen, M.; Bowles, M.; Dietrich, N.; Dubuque, T.; Geisel, S.; Kucher, T.; Lacy, M.; Le, M.; Martin, J.; Morris, M.; Thelsing, B.; Wilte, T.; Lenon, G.; Soares, B.; Milson, R.; Moore, B.; Thelsing, B.; Wilte, T.; Lenon, G.; Soares, B.; Wilson, R.; and The Mashd-HHH Mouse EST Project
Contact: Marra Mayouse EST Project
Mashlington University School of Medicinep
Mashlington University School of Medicinep
Hell 266, 1890
Per; J14, 266, 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //issue_type="carcinona"
//lab_host="soln (kananycin resistant)"
//lab_host="soln resistant"
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:651487"
/clone_lib="Stratagene mouse embryonic carcinoma (#937317
seq_documentation_block:
LOCUS AA215070 557 bp mRNA EST 03-FEB-1397
DEFINITION wu/5f04.r1 Stratagene mouse embryonic carcinoma (#937317) Mus
musculus cona clone IMAGE:651467 5' similar to gb:M38188 OVARIAN
GRANILOSA CELL 13.0 KD FROTEIN HGR74 (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: notes severation. wustl. edu
This clone is available royalty free through LINI.; contact the
This clone is available royalty free through LINI.; contact the
This clone is available royalty free through LINI.; contact.on.
This clone is available royalty free through LINI.; contact.on.
This clone is available to available to available the stop: 447.

Location.to.analitiers
Location.to.analitiers
Aparel - taxon.i0090*
```

```
The mark marked to the control of the community. Place of the community of the control of the community of the community of the community of the community. The control of the community of the community of the community of the community of the community. The control of the community of the community of the community of the community of the community. This close set the community of the community
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilbraties"
// Jab. horse."Vector: pSPORTI; Site_1: SalI; Site_2: NotI; This clone is among a rearrayed set of 15,47 clones from 11 clone is among a rearrayed set of 15,47 clones from 11 embryo cDNA libraties (including preimplantation stage embryos from unfertilized egg to blastocyst, embryosic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryosic extraembryonic part of E7.5 embryosic part of E7.5 embryosic ovary CONA library. Average lineart size 1.5 kb. All source libraries are cloned undiffrectionally with Oligo(dT): Not primars References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryousling a 15,000 mouse developmental CDNA matricaria, 2000, proc. Natl. Acad. Sci. U. S.A. 97: 917-9121; (2) Large-scale conv. ann.ysis reveals phase gene expression patterns during preimplantation mouse develolpment, 2000, Development, 127: 1771-17149; (3) Genome-wide mapping of US-elay mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Nol Genet 7: 1967-1978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1.539
/organism-Hus musculus*
/organism-Hus musculus*
/organism-Hus musculus*
/ordanism-GyBL/6d-
/db_xref="taxon:10090"
/clone_lib="wir Mouse 15K cDNA Clone Set"
/orsa="Clones arrayed from a variety of cDNA libraries*
/libraries*
                                                                                                                                                                   BEO088461.1 599 bp mRNA EST 26-JAN-2001 H3153D07-5 NIA Mouse 15K CDNA Clone Set Mus musculus CDNA clone H3133D07 5', mRNA sequence. BGO88461.1 GI:12571025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 TGATGAATTCTGCCTTATGCCT 505
                                                                                             seq_name: gb_est2:BG088461
                                                                                                                                                       seq_documentation_block:
LOCUS BG088461
DEFINITION H3153D07-5 NIA
                                                                                                                                                                                                                                                                                                                                                          house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 314 286 1810
Mahali mouseestébano, wustl.edu
This clone is available royalty free through LLNL; contact the
This clone is available royalty free through LLNL; contact the
TMAGE Consortium (infoélmage.llnl.gov) for further information.
WGT: 2250 ETPT.mer
Seq Primer: ETPT.mer
High quality sequence stop: 348.
Losation/Qualifiers
                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="5784"650"
/dlo.ref="taxon:10090"
/clone="IMAG:373872"
/sex="LikAG:20stes mouse embryo NDME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 nGlyGluGluAspArgProValGlyGlyGlyGluGlyH1sGlnProAlaG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 gGlnMetAsnAspGlyLeuGlyGlyAspGlyAspAspMetGluMetPheM 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 AsnCysLeuArgIleLeuMetGlyGluLeuSerAsnHisHisAspHisH1 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
Quality: 688.00 Length: 124
Ratio: 5.548 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: W64711 from: 1 to: 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 sAspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-327-750D-12 x W64711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165
                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                              FEATURES
```

```
MC) ... 3447
Ser_primer: -40RP from Gibco
Hirly quality sequence stop: 456.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 TGATGAATTCTGCCTTATGCCT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 sAspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est1:AW476468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organs="Mus musculus"
/organs="Mus musculus"
/deran="CSPIsh/64"
/db.xera="Lib="Soares mouse embryo NbWEI3.5 14.5"
/clone="InMestation"
/clone="InMestation"
/clone="InMestation"
/clone="InMestation"
/clone="InMestation"
/clone="InMestation"
/derange="In": 14.5dpc total fetus"
/derange="In": 14.5dpc total fetus"
/derange="In": 14.5dpc total fetus"
/derange="In": 15.45dpc total fetus"
/derange="In": 15.45dpc total fetus
/note="Inmediath Not I: -0.1490/dr) primer [5"
/derange="Inmediath Not I: -0.1490/dr) primer [5"
/derange="In": 15.45dpc mounts of mRNA from 2.13.5dpc and 2.13.5dpc mounts of mRNA from 2.13.5dpc and 2.14.5dpc manuscos (Pharmacia), digested with Not I and 2.14 and 2
ESM Mus musculus

BOLRAYORS, Metzoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Manmalia; Eutheria; Rodentia; Sciurognath; Muridae; Musina

1 (bases 1 to 616)

Marker, H. Hilliar, L., Allen H., Bowles H., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba T., Lacy, M., Le M., Martin, J., Morris, M.,

Geisel, S., Kucaba T., Lacy, M., Le M., Martin, J., Morris, M.,

Theistogs, R., Wille, T., Lennon, G., Soares, B., Wilson, R. and

Handlenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Handlenberg, K., Steptoe, M., Tan, P., Wilson, R. and

Handlenberg, R., Project

Contact: Marker Widouse EST Project

Asinington University School of Medicinep

Mashington University School of Medicinep

Rasinington University 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 TGGACAGGAAGACCGCCCTGTGGGAGGAGGTGAGGGCCACCAGCCTGCTG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 nGlyGluGluAspArgProValGlyGlyGlyGluGlyHisGlnProAlaG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Purative full length read vector to vector length is 617 Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: W81757 from: 1 to: 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M.Fatima Bonaldo
159 a 159 c. 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-327-750D-12 x W81757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Source
                  ORGANISM
                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
```

```
Eukaryotuka Meraza, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryotuka Meraza, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota Meraza, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 628)

10 (content of the //www.nobi.nh.nth, gov/noicgap.

11 (mono Gane Index Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gane Index (1997)

12 (content: Rober Stausberg, Ph.D.

13 (content: Rober Stausberg, Ph.D.

14 (content: Rober Stausberg, Ph.D.

15 (content: Rober Stausberg, Ph.D.

17 (content: Rober Stausberg, Ph.D.

18 (content: Rober Stausberg, Ph.D.)

18 (content: Rober Stausberg, Ph.D.)

19 (content: Rober Stausberg, Ph.D.)

20 (content: Rober Stausberg, Ph.D.)

21 (content: Rober Stausberg, Ph.D.)

22 (content: Rober Stausberg, Ph.D.)

23 (content: Rober Stausberg, Ph.D.)

24 (content: Rober Stausberg, Ph.D.)

25 (content: Rober Stausberg, Ph.D.)

26 (content: Rober Stausberg, Ph.D.)

27 (content: Rober Stausberg, Ph.D.)

28 (content: Rober Stausberg, Ph.D.)

29 (content: Rober Stausberg, Ph.D.)

20 (content: Rober Stausberg, Ph.D.)

20 (content: Rober Stausberg, Ph.D.)

20 (content: Rober Stausberg, Ph.D.)

27 (content: Rober Stausberg, Ph.D.)

28 (content: Rober Stausberg, Ph.D.)

29 (content: Rober Stausberg, Ph.D.)

20 (content: Rober Stausberg, Ph.D.)

21 (content: Rober Stausberg, Ph.D.)

22 (content: Rober Stausberg, Ph.D.)

23 (content: Rober Stausberg, Ph.D.)

24 (content: Rober Stausberg, Ph.D.)

25 (content: Rober Stausberg, Ph.D.)

26 (content: Rober Stausberg, Ph.D.)

27 (content: Rober Stausberg, Ph.D.)

28 (co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), and digested with Not I and clond into the Not and Eco RI sites of the modified pf/73 vector. Library ewert through one round of normalization, and was exert through by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block: 628 bp mRNA EST 24-FEB-2000 LOCOS ANG 6168 NO CORP. 24-FEB-2000 ANG 6168 NO CORP. 24-FEB-2000 ANG 6168 NO CORP. 24-FEB-2000 SERVING ANG 6168 NO CORP. 25-2097027 SY SERSION OF ANG 64 MRNA sequence. ACCESSION ANG 7648 MRNA sequence. PERSION ANG 7648 NO CORP. 25-209. SERSION ANG 7648 NO CORP. 25-209. SERSION ANG 7648 NO CORP. 25-209. SERSION ANG 7648 NO CORP. 25-209. SERSION. ANG 7648 NO CORP. 25-209. SERSION.
```

```
MashU-HHMI Mouse EST Project
MashIngton University School of MedicineP
Tashington University School of MedicineP
Tashington Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
MINISTRATION TO THE PROPERTY OF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAlaAsnValHisGlnGluAsnGluGluMetGluGlnProLeuGlnAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 ATGGCCAATGTCCACCAGGAAACGAAGAGAGAGAGCAGCAGCCCTGCAGAA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 nGlyGluGluAspArgProValGlyGlyGlyGluGlyHisGlnProAlaG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 124
Gaps: 0
Percent Identity: 97.581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AA253897 from: 1 to: 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 sAspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
Quality: 687.00
Ratio: 5.540
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-327-750D-12 x AA253897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Managerian Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manabla; Euteleostomi; Manabla; Euteleostomi; Manabla; Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 468)
Marrae, Hiliser.L., Allen, M., Bowles, M., Dierrich, M., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B., Theislang, K., Steptoe, M., Tan, P., Underwood, K., Moore, B., Thaislang, M., Willson, R. and Materston, R. MashU-HMNI Nouse EST Project
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA233897 468 bp mRNA EST 13-MAR-1897 m931e10.tl Barstead mouse pooled organs WIDER4 Wus musculus cDNA colone IMAGE:69482 5' similar to gb.M38188 OVARIAN GRANULOSA CELL AAA23897 CF PROTEIN HGR?4 (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 AATTGTCTACGCATCCTTATGGGGGAGCTGTCTAACCACCACGATCACCA 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 AsnCysLeuArgIleLeuMetGlyGluLeuSerAsnHisHisAspHisH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 lyasnasnasnasnasnasnHisasnHisasnHisasnHisaHisargarg 50
                                                                                                                                                                                                                 alignment_scores:
Quality: 688.00
Guality: 5.548
Percent Similarity: 100.000
Percent Identity: 98.387
                                                                                                                163 t
                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AK004531 from: 1 to: 809
                                                                                                                    Б
             790. .795
/note-"putative"
809
                                                                                      /note-"putative"
208 a 211 c 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 sAspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-327-750D-12 x AK004531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est1:AA253897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seg_documentation_block:
LOCUS AA253897
DEFINITION my31e10.rl Ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
Mus musculus
                polyA_signal
                                                               polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
```

```
117 sAspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est1:AW908751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organs="Mus musculus"
/organs="Musculus"
/organs="Musculus"
/clone_lib=Soares_mammary_gland_NMLNG"
/clone_lib=Soares_mammary_gland_NMLNG"
/tissue_type="mammary gland"
/lab_post="philob"
/lab_post="philo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Divaryota, Wetazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I bases 11 of 450)
Harra M., Fillier, L., Allen, M., Bowles M., Detrich, N., Dubuque, T., Getsel, S., Kucaba, T., Lacy, M., Lew, Martin, T., Martin, T., Martin, Martin, Martin, M., Morte, M., Martin, Martin, M., Morte, M., Martin, Martin, M., Morte, M., Martin, M., Morte, M., Martin, M., Morte, M., Martin, M., Morte, M., Materson, R., Morte, M., Materson, R., Malle, T., Lennon, G., Soares, B., Milson, R. and Materson, R., Milson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WaterBroon, R.
The WashO-HRIM Mouse EST Project
Unpublished (1996)
Contact: Marta MyMouse EST Project
WashU-HRIM Mouse EST Project
WashU-HRIM Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 316 286 1810
Fax: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS AII53323 430 bp mRNA EST 30-SEP-1998
DEFINITION U477940.1 Sorges_mammax_ye_fland_NNLMC Mus musculus CDNA clone
IMAGE:1477034 5' similar to gb:#38188 OYARIAN GRANULOSA CELL 13.0
KD PROTEIN HGR74 (HUMAN);, mRNA sequence.
Quality: 681.00 Length: 124
Ratio: 5.537 Gaps: 0
Percent Similarity: 99.194 Percent identity: 97.581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: Al152323 from: 1 to: 430
                                                                                                                                                                                                                 117 sAspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                         528 TGATGAATTCTGCCTTATGCCT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI152323
AI152323.1 GI:3680792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-327-750D-12 x AI152323
                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_estl:AI152323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS Al152323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
```

```
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. B. Norl-Capa http://www.ncbi.nlm.nih.gov/ncicgap; Norl-Capa Lancer Institute, Cancer Genome Anatomy Project (CGAP); Tumor Gene Index Dipublished (1997).

L. Unpublished (1997).xl
Contect: Robert Strausberg, Ph.D.
Email: Gapaba-Fafeali.nlh.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                force—"Vector: pf773D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from mammary gland tissue from a lacteting female, and was then primed with a Not I - oligo(d7) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:

ANGORDY
ANGORDY
ANGORDY
ANGORDY
ANGORDY
ANGORDY
ANGORDY
ANGORD
ANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol:194227
Mol:194227
Mol:194229
High quality sequence stop: 468.
Location/Qualiflers
1. 503
/Organism-Mus musculus*
/Organism-Mus musculus*
/Organism-Mus musculus*
/Clone-Inb-NSOares_mammary_gland_NMLMG*
/Issue_type-'mammary gland*
/lab_hoge-'mammary gland*
34 lyAsnAsnAsnAsnAsnHisAsnHisAsnHisAsnHisHisArgArg 50
```

```
110000 .1 Continuation (2 of 11)
15759 ! L39996 Azorobacter vinel
3000 ! AJ251864 Folypocladium in
10612 ! AE002479 Neisseria menin
329861 ! ALI62756 Neisseria meni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The following selection criteria; matched man 91: 705/049.

L. 793

Action Add Lifers

Add Laref "texton: 8606"

Add Laref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USAN CONTACT: MGC help deak
CONTACT: MGC help deak
CONTACT: MGC help deak
Email: cgapba-refemail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The LI M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Caneer Agency, Vancouver, BC, Canada
infoébogse.bc.camparation Readom Chiu, Chiris Pjell, Ein Garland, Ren Guin,
Sisanna Chan, Readom Chiu, Chiris Pjell, Ein Garland, Ren Guin,
Letticia Hislao, Martin Krzywinski, Reta Kusche, Oliver Lee, Soo
Sen Lee, Viccor Ling, Carrie Marhewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvanch Saeedi, Jacquellne
Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranda Tsai, Natros Warra,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.N.G.E. Consortium/Link at: http://image.lnh.gov
Series: IRAL Pates: 6 Row: K Column: 22
This clone was selected for full length sequencing because it the passed the following selection criteria: matched mRNA gl: 7657043.
                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOGIS
ECO1919
FINITION Homo saplens, p75xNR-associated cell death executor; ovarian
DEFINITION Homo saplens, p75xNR-associated cell death executor; ovarian
granulosa cell protein (13KD), clone MGC:802 IMAGE:3357965, mRNA,
ACCESSION BC003199
WERSION BC003190.1 GI:13112030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Mankaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Solumisation
Submitted (13-FBE-2001) National Institutes of Health, Mammallan
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
     1.0e+03
299.25
82.39
256.15
5.6e+03
     107.47
117.18
127.24
118.39
94.33
     91.00
88.50
87.50
87.50
                                                                                                                                                                                                                                                            seq_name: gb_pr:BC003190
9b_htg:LMFLCHR16_01
9b_ba:aVIALGEB
9b_p1:TIN251864
9b_ba:AE002479
9b_ba:NMA522491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REMARK
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Len | Documentation | 1920 | 1931 | 1820 | 1931 | 1820 | 1931 | 1821 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1931 | 1
                                                                                                                                                                                                                                                                                        Command line parameters:
-WODEL-frame-Dail, model -DEV-XIh
-WODEL-frame-Dail, model -DEV-XIh
-WODEL-frame-Dail, model -DEV-XIh
-WODEL-frame-Dail, model -DEV-XIh
-WODEL-FRAME-DAIL -DEVENTAL -DEVENT
                                                                                                                                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
           out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The state of the s
     OM of: US-09-327-750D-13 to: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search information block:
Query: US-09-327-7500-13 .
Query length: 1111
Database sequences: 1472140
Database length: -341344837
Search time (sec): 4557.230000
                                                                                    Date: Mar 11, 2002 3:33 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strd 0
+ 6
+ 6
```

```
2 (Bases 1 to.700)
Mukal, J., Hachlya, T., Hoshino, S., Kimura, M., Nadano, D., Suvanto, P.,
Mukal, J., Hachlya, T., Irie, S. and Sato, T.
Direct Submission
Submitted (17-SEP-1999) otolaryngology/Pathology, Columbia
University, G30 West 168th St., P&S 11-451, New York, NY 10032, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /ilainslation="kanyhqqrreeriopilomgordrygggegegeprannnnhhh
hinhhrqoarilapirnhh pnromnoilgedgeddebwfweemreirrkilreloling
lriliadeslonhidhedreclap
                                                                                                                        Eukaryora, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia: Euteleostomi, Mammalia: Euteleostomi, Mammalia: Euteleostomi, Mammalia: Euteleostomi, Mammalia: Euteleostomi, Musica, Musi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"involved in the common neurotrophin receptor pSWR*mediated signal transduction; NADE codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="p75NTR-associated cell death executor"
/protein_id="AAF75131.1"
/db_xref="G1:8452898"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 CAAACAACAACAACAACCACACATAACCACAACCACCACGGAAGA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 lyAsn.....ArgArg 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 etGluGluMetArgGluIleArgArgLysLeuArgGluLeuGlnLeuArg 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 'o: AF187066 from: 1 to: 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/organism="BALB/c"
/db_xref="taxon:10090"
1. 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Nade"
             AF187066.1 GI:8452897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177. .551
/gene="Nade"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block
US-09-327-750N-23 x AF187066
         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
20298829
2 (Dases I to 891)
2 (Dases I to 891)
Wikit, J., Hachiya, T., Hoshino, S., Kimura, M., Nadano, D., Suvanto, P., Hanaoka, T., Li, Y., Irie, S. and Sato, T.
Direct Submission
Direct Sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 act documentation block:
10-000
DEPINITION MUS musculus p75NTR-associated cell death executor (Nade) mRNs, accession AF18706 ACCESSION AF18706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 111
Gaps: 0
Percent Identity: 100,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AF187064 from: 1 to: 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 HisAspHisHisAspGluPheCysLeuMetPro 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                612 CATGACCATCATGATTTTTGCCTTATGCCT 644
                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
1. .891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 9
                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="NADE"
312. .647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality: 609.00
Ratio: 5.486
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-327-750D-13 x AF187064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_ro:AF187066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                  MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                          dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                   FEATURES
```

```
68 lullephemetGluGlumetArgGlulleArgArgLysLeuArgGluLeu 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-327-750D-13 x G72708/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_geores:
Quality: 418.00
Ratio: 5.429
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                 Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STS
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Publication of the property of
/translation='meoplowocedryorgededhopaannnhhhhhhhhhhhhh
RROQARHAPRRAAIPROMUGGGGGDGDDMEWFMEENREIRRKLRRLQLRNCLRIL
MELSHHDHHDEGLAP
110 c 136 g 111 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G72708 421 bp DNA STS 08-AUG-2001
MARC 4953-4954:991939031:1 SCP · porcine spleen Sus scrofa STS
genomic, sequence tagged site.
G72708.1 G1:15146738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 .....Arg 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Freking BA
USDA, ARS, US Meat Animal Research Center
PO Dax 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4278
                                                                                                                                                                                                                         alignment_scores:
Quality: 538.50 Length: 125
Ratio: 5.080 Gaps: 1
Percent Similarity: 84.800 Percent Identity: 79.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AF187065 from: 1 to: 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-327-750D-13 x AF187065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seg_documentation_block:
LOCUS G72708
DEFINITION MARC 4953-495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_sts:G72708
                                                                                                    142 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
```

```
The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence des not necessarily represent the entire amplicon. Sequence derived from POLYPHEG was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score electrophoses is.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 others
                                                                                                                                                                                                                             Template: 50-200 ng genomic DNA each 20 pmoles cach 20 pmoles dWTPs: each 88 uM Taq Polymerase: 0.25 units (Qiagen HotStar)
                                                                                                                                                                                                                                                                                                                                  Buffer:
Commercially supplied Giagen HotStar buffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 77
Gaps: 0
Percent Identity: 98.701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: G72708 from: 1 to: 421
                                                                                                              Hotstart: 95 degrees for 15 minutes
Denature: 95 degrees for 30 seconds
Anneal: 56 degrees
Extension: 68 degrees for 2 minutes
Cycles: 32 to 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 t
Pax: 402 762 4173
Emall: frekingemall.marc.usda.gov
Briner A: GCAAAVTGGGTGAAACTCTACT
Primer B: CCAGCAGCAAATAGACG
PTS alze: 500
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualiflers
```

```
1.1229
/organism-*Homo sapiens*
/db_cref="texon:9606"
/db_cref="texon:9606"
/clone="texon:9606"
/clone="texon:9606"
/clone="texon:9606"
/clone="texon:9606"
/clone="texon:9606"
/clone="texon:9606"
/clone="texon:9606"
/codon=stref="texon:9606"
/codon=str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
Bown sapiens
Bown Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 euGlnLeüargAsnCysLeuargileLeuwetGlyGluLeuSarManHis 100
480 AGCAGATGAGGACATATAGGGCTTGCAAACTCCTGAACCTGAGAACAT 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 tGlullePheMetGluGluMetArgGluIleArgArgLysLeuArgGluL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 IleProAsnArgGlnIleAsnAspGlyMetGlyGlyAspGlyAspAspMe 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AsnIleHisGlnGluAsnGluGluMetGluGln...ProMetGlnAsnGl 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
Quality: 277.00 Length: 111
Ratio: 3.298 daps: 4
Percent Similarity: 75.676 Percent Identity: 54.955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AK000959 from: 1 to: 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 HisAspHisHisAspGluPheCysLeuMetPro 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq documentation_block:
LOCOS XXIOO213 1364 bp DNA
LOCOS XXIOO221 32 from Patent WO0119660.
ACCESSION AXIOO231 GI:13539115
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      530 TATGAC.....TITIGCCTCATACCT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-327-750D-13 x AK000959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_pat:AX100231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION VERSION VERSION VERSION VERSION VERSION CERVINCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E 15091. Tand CASEALT.

Direct Submission

Direct Submission

Submitted (16-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takao

Submitted (16-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takao

Submitted (16-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takao

Kisarzau, Chiba 292-0812, Japan (E-mall:genomics@hri.co.jp,

Tel:81-418-52-3931, Fax:81-438-52-3952)

NEDO human CDNA sequencing project supported by Ministry of
International Trade and Industry of Japan, CONA full insert

sequencing: Research Association for Biotechnology; CDNA library

construction, 5. e 3'-end one pass sequencing and clone selection:

Helix Research Institute (Supported by Japan Key Technology Center

etc.) and Department of Virology, Institute of Medical Science,

University of TOKYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block: 1229 bp mRNA PRI 22-FEB-2000
LECOUS AKO0059: 1229 bp mRNA PRI 22-FEB-2000
DEFINITION Hom Sapiens CDNA FLJ10097 fis, clone HEMBA1002458, weakly similar to OMMARAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.
ACCESSION AKO00959 AKO00959 IG:7021945
NEETWORN AKO00959 IG:7021945
SOURCE Home Sapiens embryo. 10 weeks whole embryo, mainly head cDNA to SOURCE Home Sapiens embryo. 10 weeks whole embryo. mainly head cDNA to REPRENCE Home Sapiens Chordata; Craniata; Vertebrata; Euteleostom!; Mammalia; Butherla; Primates; Catarrhini; Hominides; Homo. REPERRICE I (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogair., Ota.T., Hayashi.K., Sugiyama,T., Otsuki,T., Suzuki.Y.,
Nishikawa,T., Ragai,K., Sugano,S., Takahashi-Fulii,A., Hara,H.,
Tanasa,T., Nomitar,Y., Togiyar,S., Yomani.F., Hara,R., Yakahuchi.K.,
Arita,M., Mobkura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Hakamarisu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.
Unpulished (2000)
2. (bases i to 1229)
Isogai,T., and Otsuki,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 alalleProAsnArgGlnIleAsn.....AspGlyMetGlyGlyAsspGl 64
19600 GATGTGCCCAATAGGCTTGTCGATAACATGAAATGATGAGAGTGG 19649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19506 GAAT.....GAAGCCCCCGCTTTAGGAGGTGGTGAATACCAGGAGCCTG 19549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::||||||| :::||||
19550 GAGGAAATGTTAAAGGGGTTTGGGCTCCACCTGCCCCGGGTTTTGGAGAG 19599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 nAsnGlyGluGluAspArgProLeuGlyGlyGluGlyHisGlnProA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 laGlyAsnArgArgGlyGlnAlaArgArgLeuAlaProAsnPheArgTrp 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 euArgGluLeuGlnLeuArgAsnCysLeuArgIleLeuMetGlyGluLeu 97
                                                                                                                                                                                                                                                                                                                                                                                      1 MetalaasnileHisGlnGluAsnGluGluMetGluGln...ProMetGl 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 4
Percent Identity: 57.018
                                                                                                                                                                                                                                                                                     Align seg 1/1 to: HSV351F8 from: 1 to: 45678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualiflers
                                                                                                                                                                  alignment_block:
US-09-327-750D-13 x HSV351F8
                        Ratio: 3.571
Percent Similarity: 73.684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_pr:AK000959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
```

PAT

```
"LINC/D repeat: matches 4646, .5565 of consensus" . 15909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       norde "METATA repeat: matches 295. .487 of consensus"
2034. . 20692
                                                                                                                                                                                                                                                             repeat: matches 1357. .1972 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -*AluJb repeat: matches 136. .295 of consensus" . .16953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e="Alusc repeat: matches 118. .295 of consensus"
4. .18175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat: matches 977. .1357 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ce="MuTiD repeat: matches 201. .241 of consensus"
78. .14240
ce="AluSg1 repeat: matches 1. .270 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --1.12 repeat: matches 4499, .4619 of consensus"
. 17377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note-"MLTID repeat: matches 177. .505 of consensus"
                                                                                                                                                                                                                                                                                                Anote-"Firm A repeat: matches 2, .129 of consensus" 11572, .11946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ce-"Alusx repeat: matches 24. .312 of consensus"
59. .16363
2 repeat: matches 1676. .1720 of consensus* 478
                                                                                                                                                                                                                                                                                                                                                                                                             e="LLMD repeat: matches 275. .977 of consensus"
4. .13223
                                                                                                                                                                                                                                                                                                                                                                                                                                                   - "LIMD repeat: matches -17. .113 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##AlumbB repeat: matches 1, ,318 of consensus" ,18298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /hote="AluSg repeat: matches 1. .302 of consensus" 20701. .20809
/hote="LTR1 repeat: matches 682. .785 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           // 1025 | 11/10 repeat: matches 2, .201 of consensus // // 1024, .15604
                                                                                                             te-"Aluxb8 repeat: matches 1. .316 of consensus"
                                                                                                                                                                                note="309 of consensus" note="309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15. .14534
e="Alusc repeat: matches 1. .290 of consensus"
15. .1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e="Alusx repeat: matches 1. .291 of consensus"
2. .16641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 1. .284 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Alusc repeat: matches 1. .118 of consensus"
18848. .18873
1676e-"13 copies 2 mer tg 100% conserved"
                                                                          repeat: matches 239. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 1, .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat: matches 1, .295 of consensus"
                                                                                                                                                                                                                          repeat: matches 99. .212 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat: matches 5. .292 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 copies 2 mer tg 100% conserved"
19171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e- 25 coples 2 mer ac 100% conserved* 6. 19533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="26 copies 2 mer at 79% conserved"
17704. 17863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           = "55 copies 2 mer ct 77% conserved"
                                                                                                                                             copies 2 mer aa 81% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-"AluSx
                                                                                                                                   7952. .7987
/note="18 co
7990. .8305
                                                                                                                                                                                                                                                                                                                                   e "LIMD
                   repeat_region
                                                                                              repeat_region
                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                           repeat_region
                                                                                                                                   repeat_region
                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
```

```
4 repeat: matches 5360, .5434 of consensus<sup>*</sup>
600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27536. .27600
//note="LIMA repeat: matches 2220. .2283 of consensus"
27601. .27975
                                                                                                                                                                                                                                                                                                                                                                                      25959. .26012
/note="HERVFH21 repeat: matches 23. .79 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat: matches 137. .289 of consensus"
                                                               7.071-1. .22074 repeat: matches 409. .543 of consensus'
                                                                                                                                                                                                                                                        /note-'Alusgi repeat: matches 1. .308 of consensus' 4265. .2407.

2274. .2580.

2274. .2580.

2581. .2581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-'Mir repeat: matches 92. .191 of consensus' 7.016-'Mir repeat: matches 92. .191 of consensus' 7.016-'Mir repeat: matches 1. .131 of consensus' 2.2583 .23624 .23624 .23632 .23634 .23635 .24641
                                     5. .21636
e-"LTR29 repeat: matches 3. .498 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                            44...26456
hte-"Alur repeat: matches 1. .311 of consensus"
1. .27432
                                                                                                       luY repeat: matches 2. .308 of consensus" 22974
RI repeat: matches 1, .195 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64388 AGAAGAATCCCGCCATTTGGAGGGGGTGAAGGCCAGAAGCCTGGAGGAA 64437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64532 AGAAAGGTTTGTAGGGCAGATGATGGAAATCAAGAGAAAGACTAGGGAAC 64581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 euglnLeuArgAsnCysLeuArglleLeuMetGlyGluLeuSerAsnHis 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 sn...ArgArgGlyGlnAlaArgArgLeuAlaProAsnPheArgTrpAla 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 yGluGluAspArgProLeuGlyGlyGlyGluGlyH1sGlnProAlaGlyA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 IleProAsnArgGlnIleAsnAspGlyMetGlyGlyAspGlyAspAspMe 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 tGluIlePheMetGluGluMetArgGluIleArgArgLysLeuArgGluL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 111
Gaps: 4
Percent Identity: 54.955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: HS635G19 from: 1 to: 69648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 HisAspHisHisAspGluPheCysLeuMetPro 111 :::[|] :::[|] 64632 TATGAC......TTTTGCCTCATACCT 64652
                                                                                                                                                                                                                                                                                                                                                                   'note-"match: GSS B63622"
                                                                                                           /note-"Alux 1
22878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluJb
27436. 27507
/note="L1M4 r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277.00
3.298
75.676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-327-750D-13 x HS635G19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality: 2
Ratio: 3
Percent Similarity: 7
repeat_region
                                repeat_region
                                                                   repeat_region
                                                                                                                                       repeat_region
                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                       repeat_region
                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                 misc_feature
```

repeat_region 1865718871 /note="MIR repeat: matches 35252 of consensus" renest realth 182719230		repeat_region 1949219959 /note="MIR repeat: matches 267 of consensus"	repeat_region 1956019621 /note="Alux repeat: matches 34295 of consensus"	repeat_region 1982219959 // note="MIR repeat: matches 67212 of consensus"	repeat_region 1998720286 / natches 1300 of consensus / nore="AluX repeat; matches 1300 of consensus"	repeat_region 20316. 20512 /note="MIR repeat; matches 82, .262 of consensus"	repeat_region 20213. 20741	repeat_region 2009, 12,000	repeat_region 71085. Instance 1776 1888 of consensus*	repeat_region 21212, 21318	repeat_region 21392. 21471	/note="Mrk repeat; matches 3, .do ut consensus repeat_region 22146, .22441	/note="AluSx repeat: matches 1296 or consensus repeat region 2252622610	repeat region 2294023204	/note="HERVIE repeat: matches 378, .650 of consensus"	repeat_region 2320523514 /note="AluSq repeat: matches 1311 of consensus"	repeat_region 2391924194 //note="AluSx repeat: matches 36311 of consensus"	repeat_region 24496. 24590	repeat_region 24871, 12436 repeat matches 102 143 of consensus	repeat_region 25378, 25555	repeat_region 25673, 25910	/note="MIR repeat: matches 4255 of consensus repeat_region 2672226798	/note="L2 repeat: matches 2572, .2649 Of 27040, .27107	/note="12 repeat: matches 24892500 of 2710827374		repeat_region (17): 2.17.1 matches 23722489 of consensus"	" \ (repeat_region 289/52909/ /note="MER96 repeat: matches 42173 of consensus"	repeat_region 29173. 29196 /note="12 copies 2 mer am 100 conserved"	misc_feature 29832, 30260	repeat_region 70392. 30597	repeat_region 30855, villal accest, matches 2 162 of consensus	/note="MEK91B repeat: matches 4102 of consensus repeat_region 3105631094	/note-"MIR repeat: 3172831791	/note="16 copies 4 3185831952		/note="match: STS	repeat_region 3304333033
	/note="14 copies 2 mer ac 100 conserved" 183, ,258					repeat_region 5036. 5486 /note="LIMEc repeat: matches 20522207 of consensus"		c	<pre>misc_feature complement(71877611) /note="match: GSS: Em:AQ566001"</pre>	repeat_region 7369, 7594 /note="MIR repeat: matches 34, .256 of consensus"		repeat_region 79047978	, 4	/note="MIR repeat: matches 8255 or consensus" misc_feature 8154, .8555				c		repeat_region 1013510428 /note="AluSx repeat: matches 1294 of consensus"	repeat_region 10429, .10563 /note="AluSq/x repeat; matches 1, .135 of consensus"	2705 of o	repeat_region 10819, 11050	repeat_region 11112. 11324	/note-"MIR repeat: matches 11255 Or consensus- repeat_region 1186912012	/note="MIR repeat: matches 20167 of consensus" repeat_region 12925, .13223	/note="Alux repeat: matches 1300 of consensus" repeat region 1329013495	/note-*MERSBA repeat: matches 9214 of consensus*	/note="match: GSS: Em:AQ568864"	repeat_region foote="Miss repeat: matches 77, .139 of consensus" foote="Miss repeat: matches 77, .139 of consensus foote="Miss repeat: matches 77, .139 of consensus foote="Miss repeat: matches 77, .139 of consensus foote="Miss repeat:	repear_region 13040 .13500 /note-"MIR repeat: matches 22147 of consensus"	repeat_region 14162, .14245 /note="MIR repeat: matches 46, .136 of consensus"	repeat_region 14925, .15056 /note="MIR repeat: matches 48, .191 of consensus"	repeat_region 15994, .16040	repeat_region 16116, 15184	, , ,	TO STT.		

```
alignment_scores:
Quality: 194.50 Length: 113
Retio: 2.739 Gaps: 3
Percent Similarity: 62.832 Percent Identity: 43.363
HSLRAVSTDPPHHDHHDEFCLMP"
256 a 170 c 221 g 181 t
                                                                                                                                                                                                                                                   Align seg 1/1 to: AF220189 from: 1 to: 828
                                                                                                                                                                                                 alignment_block:
US-09-327-750D-13 x AF220189
                    BASE COUNT
ORIGIN
```

```
| BGB25224 602747641F1 NIH_W
| B1114083 60286118F2 NIH_M
| AM161416 au81e08 y1 Schnei!
| BE95584 601275870F1 NIH_M
| BF970435 602272771F1 NIH_M
                                                                                                                                                                                                                         N3437 159 bp mRNA EST 16-7AN-1996 yx79c03.II Soares melanocyte 2ADHW Homo saplens CDNA clone inaces:867940 5' safilar to 9b:W18188 OVARIAN GRANULOSA CELL 13.0 KD PROFISH HGR74 (HUMAN); mRNA sequence.
N34237 GI:1155379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_Scores: Length: 111
Quality: 609.00 Length: 111
Ratio: 5.486 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
           690
693
697
699
   999.39 1.7e-46
999.35 1.7e-46
999.30 1.7e-46
999.28 1.7e-46
999.25 1.7e-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: N34237 from: 1 to: 519
   + + 582.00 5
+ + 582.00 6
+ 582.00 9
+ 582.00 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-327-750D-13 x N34237
                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS N34237
DEFINITION yx79c03.rl So
                                                                                                                                                                                seq_name: gb_est2:N34237
           gb_est2:BGB25224
gb_est2:BII14083
gb_est1:AM161416
gb_est1:BE385584
gb_est2:BF970435
                                                                                                                                                                                                                                                                                                                                                                        ACCESSION PARESTON PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
SOUICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N31219 (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1975) (1
                                                                                                                                                                                           About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                  out_format : pfs
                  of: US-09-327-750D-13 to: EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search information block:
uerry: US:09-27-750D-13
Query: US:09-27-750D-13
Query: US:07:00
Carbabase : US:07:00
Carbabase : US:07:00
Carbabase : US:07:00
Search time (Sec): 4085-940000
                                                                   Date: Mar 11, 2002 2:16 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strd C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score_11st:
Speakers
```

```
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Frimates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 615)

Norl-CAP http://www.ncbl.nlm.nlh.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (GGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Emali: Gapba-Fremil.nlh.gov

This clone is available royalty-free through Link.; contact the Insert Length: 84 the Englished (1997)

Sea primer: -dung from Giboon 11nh.gov) for further information. Sea primer: -dung from Giboon 11nh.gov) for further information. Insert Length: 84 the Englished 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Homo sapiens"
/organism-"Homo sapiens"
/olone-"IthkOE:1744289
/clone-lib-"Soares_fetal_lung_NDHI199"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                    EFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                 JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/clone_lbb=NRI_CGAP_Lym12*
/clone_lbb=NRI_CGAP_Lym12*
/clone_lbb=NRI_CGAP_Lym12*
/clone_type="lymphoma, follicular mixed small and large-cell"
/lab_loss="PuH10B"
/lab
                  DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NGT-CARP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/langs/thml/itesources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 422.
1...6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
615 bp mRNA MHLISH Home 29-CCT-1998
DEFINITION qe65909.X1 Somes feeal_ling_NHLISH Home sapiens CDM clone TMAGE:1744288 1's finilar coof 90-33188 OWARIAN GRANULOSA CELL 13.0

KD_ROTEIN HGR74 (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 lyAsnArgArgGlyGlnAlaArgArgLeuAlaProAsnPheArgTrpAla 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 tGluIlePheMetGluGluMetArgGluIleArgArgLysLeuArgGluL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: AW512400 from: 1 to: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-327-750D-13 x AW512400/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est1:AI193112
                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                       FEATURES
```

```
84 euGlnLeuArgAsnCysLeuArglleLeuMetGlyGluLeuSerAsnHis 100
                                                     Align seg 1/1 to reverse of: AI193112 from: 1 to: 615
101 HisAspHisHisAspGluPheCysLeuMetPro 111
                                 alignment_block:
US-09-327-750D-13 x AI193112/rev
```

AI193112 AI193112.1 GI:3744321

human. Homo sapiens

ACCESSION / VERSION / KEYWORDS / SOURCE / ORGANISM / OR

```
/organism="Nomo sapiens"
/organism="Nomo sapiens"
/organism="Nomo sapiens"
/clone_lib="NiH;McC_lib="NiH;McC_lib="NiH;McC_lib="NiH;McC_lib="NiH;McC_lib="NiH;McC_lib="NiH;McC_lib="NiH;McC_lib="NiH;McC_lib="NiH;McC_lip="NiH;McC_lip="NiH;McC_lib="NiH;McC_lip="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_lib="Nih;McG_l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peng, Y., Song, H., Huang, O., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., X.X., Li, N., Qiao, B., Liu, F., Ou, J., Gao, X., Cheng, F., Xu, Z., Eng, F., Song, F., Yu, Z., Song, W., Tu, Y., Jia, J., Pu, G., Ren, S., Zhong, M., Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Momos, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Buteleostomi, Mammalia, Buteleostomi, Catarrhini, Hominidae, Homo. I (bases 1 to 720)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block: 720 bp mRNA EST 08-0CT-2000 LOCGS AV701506 ANY 01506 ANY 0150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: BG745809 from: 1 to: 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH_MGC Library."
186 c 142 g 179 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 HisasphishisaspGluPheCysLeuMetPro 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 CATGACCATCATGATGAATTTTGCCTTATGCCT 197
Location/Qualifiers
1. .674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-327-750D-13 x BG745809/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est1:AV701506
                   FEATURES
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name of the control o
                   enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Triset, Italy). 2 others 113 c 169 g 170 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetalaasnileHisGlnGluasnGluGluMetGluGlnProMetGlnAs 17
                                                                                                                                                                                                                                                                                                                                                                                                        Ouality: 609.00 Length: 111 Ratio: 5.466 605ps: 0.00 Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: LLCM1691 row: e column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: A1929106 from: 1 to: 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-327-750D-13 x AI929106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est2:BG745809
                                                                                                                                                                       178
                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
```

```
1. 560

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500

1. 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      And wow States Sukrycke, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Frimates, Catarrhin; Hominidae, Homo.

1 (Dases 1 to 557)
Shift-MGC Tutp://mgc.nci.nlh.gov/.
National Institutes of Health, Nammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Danali: capibs-rémail nih.gov
Tissue Procuremen: Miklos Palkovits, M.D., Ph.D.
CDNA Library Freparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Freparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Freparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Freparation: Michael J. Brownstein (NHGRI),
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution in MGC and staribution in MGC clone distribution in MGC clone distribution: MGC clone distribution in MGC manual Library Arrayed by: The I.M.A.G.E. Consortium/LLNL at:
High quality sequence stop: 567.
Location/Qualifiers

        Seq_documentation_block:
        567 bp
        mRNA
        EST
        07-MAY-2001

        LOCUS
        BG705683
        567 bp
        mRNA
        EST
        07-MAY-2001

        ACCESIN
        602668940F1 NH_MGC_96 Homo sepiens cDNA clone INAGE:4791506 5', ACCESSION
        ACCESSION
        BG705685

        VERSION
        BG705685-1
        GI:13980274
        GI:13980274

                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
Quality: 597.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est2:BG705685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.

MISM Homo saptens

Bukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoni;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 551)

MISTACHER; CM95.nci.nlh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Tissue procurement. Anc.

CONTACT: Robert Strawberg, Ph.D.

Tissue procurement. Anc.

CONTACT: Anc.

MAC.

                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCGS B648054 557 bp mRNA EST 21-MAR-2001
DEFINITION 60257934F1 NH_MGC_21 Homo sapiens CDNA clone IMAGE:4651353 5',
ACCESSION B6482054 1 GI:13414333
Align seg 1/1 to: BG482054 from: 1 to: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-327-750D-13 x BG482054
                                                                                                                                                                                                                                                                                                  seq_name: gb_est2:BG482054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
```

```
Homo saptens

Enkaryote: Metacos: Chordete; Craniete; Vertebrate; Enteleostomi; Memmalia: Entheria: Primates; Catarrhini; Hominidae; Homo.

Memmalia: Entheria: Primates; Catarrhini; Hominidae; Homo.

MIN-MCC http://mgc.nci.nih.gov/.

MIN-MCC http://mgc.nci.nih.gov/.

MIN-MCC http://mgc.nci.nih.gov/.

MIN-MCC http://mgc.nci.nih.gov/.

Enali: cgapb: refeain.nih.gov

Contect: Robert Streads.pr. Ph.D.

Enali: cgapb: refeain.nih.gov

Contect: Library Arrade by: The Lih.A.S. Consortium(Likl)

DNA Sequence stop: SGO.

Contect: Library Robert Streads.pr.

High quality sequence stop: SGO.

(App. Trefe-traxon: 9606.

(Ab. Tref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 tGluflePhemetGluGluMetArgGlufleArgArgLygLeuArgGluL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 111
Gaps: 0
Percent Identity: 98.198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 HisasphishisaspGluPheCysLeuMetPro 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: BE252272 from: 1 to: 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality: 591.00
Ratio: 5.422
Percent Similarity: 98.198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-327-750D-13 x BE252272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                     SOURCE
                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
Tel: +55-11-2704922

Pax: +55-11-270001

Bmil: asimpsontludid.org br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
PROJECT. This entry can be seen in the following URL
(NGLP)-/Aww.ludig.org.Dr/acripts/gethtmi2.pl7tl-PMO&t2-PMO-HT0911-
0807031-012-NIORE-20070-03684-1)
Seq Primer: puc | 6forward
Seq Licklener: puc | 810p: 550.

Localion/Oualifiers
Licklener: puc | 6forward
Localion/Oualifiers
Localion/Oualifier

        seq_documentation_block:
        559 bp
        mRNA
        EST
        13-JUL-2000

        LOCUS
        BE252272
        BE25272
        BE25272
        BE25272
        BE25272
        BE25272
        BE25272
        RCCESSION
        BE25272
        BE25272
        BE25272
        BE35272
        BE35272

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality: 596.00 Length: 112
Ratio: 5.369 Gaps: 1
Percent Similarity: 99.107 Percent Identity: 99.107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 sHisAspHisHisAspGluPheCysLeuMetPro 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 CCATGACCATCATGATGATTTGCCTTATGCCT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: BG993540 from: 1 to: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-327-750D-13 x BG993540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_estl:BE252272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
```

Result Ouery No. Score Match Length DB ID Description	692 98.9 700 10 676 96.6 854 10	355.8 50.8 519 10 AF187065	5 307.4 43.9 891 9 HUMOGC 5 307.4 43.9 891 9 AF187064 5 307.4 43.9 891 9 AF187064	240.5 34.4 421 II G/2/08 154.8 22.1 785 10 AF097439	9 154,6 22.1 98274 9 18574B7 259753 Human DAN 5 c 10 101.4 14.5 45678 9 HSV351F8 270719 Human DNA 5	80.2 11.5 1229 9 AKO00959 80.2 11.5 1364 6 AXIO0231	80.2 11.5 69648 9 HSG35G19 77.4 11.1 244 11 G13550	67.6 9.7 99 10 MUSCEREBL 59.8 8.5 7218 6 166494	18 58 8.3 642 9 AF183416 19 58 8.3 828 9 AF220189	58 8.3 35714 9 HS198P4 57.2 8.2 43952 9 HSU105G4 56.4 8.1 791 9 AF237783	555.8 8.0 744 555.8 8.0 744	25 55.8 8.0 3131 9 HSV8/0H8 26 55.8 8.0 41029 2 HSU80B1	54.4 7.8 504 11 G24641 54.2 7.7 40584 9 ALI33348	54 7.7 835 10 AF097438 54 7.7 838 10 AF051347	54 7.7 2269 10 AF097437 49.2 7.0 185306 2 AC013570	48.8 7.0 37224 3 AC007061 48.2 6,9 36823 9 HSU209G1	46 6.6 154577 2 AL357046 46 6.6 154959 2 AC009282	37 46 6.6 185257 9 AL355305 38 44.8 6.4 190544 9 AC005768	44.2 6.3 110000 2 LMFLCHR15_5 44.2 6.3 172200 2 AC022626	41 43.2 6.2 9211 3 AB030033 42 43.2 6.2 210321 2 AC079438	44. 42.6	5.1 160922 Z ALSIZZGG	ALIGNMENTS	REGULT 1	AFIRTON MUST AREACTES 700 bp MENA 11-70N-2000 LOCUS AFIRTON MUST ABSOCIATED CELL DERINITION MUST ABSOCIATED CELL DEATH EXECUTOR (Nade) MENA,	ACCESSION AFIBOTOS OF STREET	KEYMORDS . SOURCE house mouse.	Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCE 1 (bases 1 to 700)	AUTHOUS PURELLY, REGILIFACT, DICTALLOST, Greene, L.A. and Sato, T.A. SUVENICO, P., MARORA, T. L.I.Y. III.E.S., Greene, L.A. and Sato, T.A. TITLE NADE, a p754NTR-associated cut ldeath executor, 1s Involved in signal transduction mediated by the common neurotrophin receptor	JOURNAL J: BIOL Chem. 275 (23), 17566-17570 (2000) MEDLINE 20299829	
version	Copyright (c) 1993 · 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: March 11, 2002, 14:17:05; Search time 1319.57 Seconds (without alignments)		Title: US-09-327-750D-28 Perfect score: 700 Seminary 3 anadostrissocacascs 3 anadostrissocacascs 100	Able: IDENTITY NIC	Gapop 10.0 , Gapext 1.0	Searched: 1472140 seqs, 8248589755 residues	Total number of hits satisfying chosen parameters: 2944280	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100%	Listing first 45 summaries	Database : GenEmbl:*	2: gb_htg:* 3: qb_htg:*		5: 95-20: 6: 95-20: 7: gb pb:#			11: 90_45: 12: 90_45: 12: phsy:	15: 9D_ui: 14: 9D_ui: 15: on ba:	15: em_fun:* 17: em_fun:*	18: em_in:* 19: em_om:*	20: em_Or: 21: em_Or: 22: em_Oat:				30: em_htgo_hum:* 31: em_htgo_hum:* 32: em_htgo_lnv:*	35: em_htg_rod:* 36: em_htg_other:*	Pred. No. is the number of results predicted by chance to have a score greater than one equal to the score of the result being printed, and is derived by a naivels of the rotal score distribution.	IARIES	

셤 ò g

õ

```
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Shubission
Direct Shubission
Submitted (13-FEB-2001) National Institutes of Health, Mammallan
Submitted (13-FEB-2002) Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                       BC003190 793 bp mRNA PRI 12-JUL-2001 Homo sapiens, p75NF-associated cell death executor; ovarian granulosa cell protein (13kb), clone MGC:802 IMAGE:3357965, mE GC00319ct cds BC003190.1 GI:13112030
                                                                                                                                                        Gaps
                                                                                                                                 Similarity 86.5%; Pred. No. 6.7e-83; Similarity 86.5%; Pred. No. 6.7e-83; Significative 0; Mismatches 47; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               653 tgtgttatt 661
|| | | | |
507 CTTGGTGTT 515
                                                                                                142 a
                                                                                                                                       Query Match
Best Local Simi
Matches 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
BC003190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                             ç
                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                               5
                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wight, J. Hachiya; Hoshino,S., Kimura,M., Nadano,D., Suvanto,P., Mukal, J. Hachiya; Tie, S. and Saco,T. Lix, T. Lix, Tie,S. and Saco,T. Direct Submissor (Lix, Tie, S. Submitted (17-SEP-1999) ottolaryngology/Pathology, Columbia University, 630 Nest 168th St., FeS 11-451, New York, NY 10032, USA 11-519 and Columbia (Astrain, Sprague Dawley, Astrain, Sprague Dawley, (Ab. Xnef Texon:10116)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. (bases 1 to 519)

Mukal, J., Hachlya, P., Shoji-Hoshino, S., Kimura, M.T., Nadano, D.,
Buxal, J., Hachlya, T., Li, Y., Ifie, S., Greens, L.A. and Sato, P.A.
Swarto, P., Handoka, T., Li, Y., Ifie, S., Greens, L.A. and Sato, P.A.
By pysynch associated cell death executor, is involved in
signal transduction mediated by the common neurotrophin receptor
pysyns
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Norway rat.
Katus norwegicus
Bukaryors Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                      AF187065 519 bp mRNA ROD 11.-UUN-2000 Rattus moregicus p75NTR-associated cell death executor (Nade) MRNA, complete ctd: AF187065 AF187065.1 GI:8452895
                                                                                                                                                                                                                                               374 caggcagatgaatgacgggttgggtggagatgatgatatggaaatgttcatggagga 433
                                                                                                                                            7. Biol. Chem. 275 (23), 17566-17570 (2000)
20298829
                                                                                                                                                                                                                                                                                                                                /gene="Nade"
44. .406
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
AF187065
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                       99 99 93
10 93 93
                                                                                                                                                                    ç q
                                                                                                                                                                                                           ò
                                                                                                                                                                                                                               90 % a
                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                ò
```

õ g ò g 5 q S G ò

```
1. OSBITONIVABILITIES
1. OSBITONIVABILITIES
1. OSBITONIVABILITIES
1. OSBITONIVABILITIES
1. OSBITONIVABILITIES
312. OSBITONIVABILITIES
1. OSBITONIVABILITIE
/, 630 West 168th St., P&S 11-451, New York, NY 10032, USA cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G72708 421 bp DNA STS 08-AUG-2001
MARC 4953-4954:991339031:1 SCF - porcine spleen Sus scrofa STS
G72708 G72708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 matagemacemagammetetemteategeematgteemeeggmaaegmagget 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404 GCCTGCAGGAA-----ATCGACGGG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 cgggttggggtggagatggagatgatatggaaatgttcatggaggagatgagagatccg 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           569 tgagatocatactgtgactoccgctgtagcoctttccctcgcattttcctgacatgcctt 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76; Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 43.9%; Score 307.4; DB 9; Length 891; Best Local Similarity 78.0%; Pred. No. 3.6e-70; Matches 428; Conservative 0; Mismatches 76; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                    224 g 234 t
                                                                                                                                                                                                                                                                                                                                                                                                                 HHDEFCLMP"
182 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 689 tgttgccag 697
||||||||||||||
779 TGTTGCCAG 787
            University,
                                                                                                                                                                                                                                                                                                                                                                                                                                        251 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
G72708/c
LOCUS
DEFINITION 1
                            FEATURES
Source
                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                            gene
                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . qa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Autory, Hachlya, T., Hoshino, S., Kimura, M., Nadano, D., Suvanto, P., Hanaoka, T., Li, Y., Irle, S. and Sato, T.
Buraoka, T., Li, Y., Irle, S. and Sato, T.
Submitted (17-SEP-1999) Otolaryngology/Pathology, Columbia
                                                                                                                               ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota Metazoa, Chordata, Craniata; Vertebrata; Buteleostoml, Mammalia, Eutheria, Primates; Catarrhini, Hominidae; Homo.
I (Dasea 1 to 891)
Mikal, J., Hachlya, T., Shol; Hoshino, S., Kimura, M.T., Madano, D., Shvatio, P., Hanacka, T., Li, Y., Irie, S., Greene, L.A. and Sato, T., M.D., a p75xFR-associated cell death executor, is involved in 973xFR transduction mediated by the common neurotrophin receptor 973xFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF187064 891 bp mRNA PRI 11-JUN-2000 Memon sapiens p75NTR-associated cell death executor (NADE) mRNA, complete cds. AF187064.1 GI:8452893
                                                                                                                                                                        149 matagcaaccaggaaacaaactcatcatcatggccaatgtccaccaggaaaacgaagggct 208
284 AAACAACAGAAAAAAAATCCCATCATCATGAAATTCTCACCAGGAAAACGAAGGAT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 ccaggctcgccgacctgaccctaacttccgatgggcattcccaccaggagtgatga 388
329 ctaggctcgccgacctgacctaacttccgatgggcattcccaccaggagtgatga 388
425 AlaGcccaccaccaccaccaracctaaraccaccaraccaaraccaaracaaraca 484
                                                                                                                                                                                                                                                                     209 ggagcagcccctgcagaatggacaggaacaccgcctgtgggaggaggtgagggccacca 268
                                                                                                                                                                                                                                                                                                                                                                 389 cgggttgggtggagatggagatgatatggaaatgttcatggaggagatgagagatccg 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    485 TGGGATGGGTGGAGATGATGATGATGAATATTCATGAGGAGATGHIIIIIIIIIIIII 111 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                taaccaccacgatcaccatgatgaattctgccttatgccttgacttcggtcattcccccc 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 43.9%; Score 307.4; DB 9; Length 891; Best Locat Similarity 78.0%; Pred. No. 3.6-70; Marches 428; Conservative 0; Mismatches 76; Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. Biol. Chem. 275 (23), 17566-17570 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               689 tgttgccag 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               779 TGTTGCCAG 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
AF187064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
```

a ò

9 % a

å a õ g Page 7

윱 ò

ó g ò g ò

```
where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMBL: SV., SMISSPROT; IT., TREMEL; WP:, WORMPEP; Information on the WORMPEP annotation on the WORMPEP annotation on the WORMPEP and Library described in U-J. Kim et al. (1996) Genomics 34, 213-218

This sequence is the entire insert of clone CTA-71487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ### Conservation of the consensus of the consensus of the consensus of the conservation of the consensus of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5496, .6885
Thote-1,1,10 repeat: matches -1, .1538 of consensus*
6896, .7185
/note-12 repeat: matches 2356, .2710 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L2 repeat: matches 2356, .2710 of consensus"
complement(7187, .7611)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /x repeat: matches 1. .135 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 repeat: matches 2648. .2705 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 2619. ,2749.of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     849 .8864 // Octe-*Alusx repeat: matches 1. .280 of consensus* complement(887 . 9290) // Conte-*Alusx repeat: Em:AQ343214*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 1. .294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat: matches 11, ,255 of consensús"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //vote="MIR repeat: matches 2, .255 of consensus" //octe="MIR repeat: matches 2, .255 of consensus" //octe="MIR repeat: matches" //octe="MIR repeat" matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 8. ,255 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atch: GSS: Em: AQ284832"
10428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8154, 8565
/note="match: GSS: Em:AQ059599"
8549, 8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Homo saplens"
/db_xref-"taxon:9606"
/chromosome-"22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .10868
lote="L2 ren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR ren
8154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29. .10563
te-"AluSq/x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="12 rr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note-"AluSx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Direct Submission
Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (18-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
CBNO 1874, UK. E-mail enquires: hunguery@sanger.ac.uk Clone
requests: clonerequestesanger.ac.uk
On Apr 8, 1998 this sequence version replaced 91:2578134.
This sequence has been finished according to sequence may acquence has been finished according to sequence as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was generated from part of bacterial clone contigs of Muman chromosome 22 constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at http://www.sanger.ce.iv/MfQC/Chr2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HS714B7 98274 bp DNA PRI 12-DEC-1999
Human DNA sequence from Glone CTA-714B7 on chromosome 25421.2-13.2
CODEALIAB pseudogene similar to part of COXTB (cytcofhrome c oxidase
subunit VIIb), a novel pseudogene, ESTs, STS and GSSs, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Admmalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
L (bases 1 to 98274)
                                                                                                                                                                 76 attgactggaagccgagagtccaggcggcagcgggaattgacaggaggactacgccgcaa 135
                                                                                                                                                                                                                                   136 gggataggccca-gaatagcaaccaggaaacaaaatctcatcatggccaatgtccaccag 194
                                                                                                                                                                                                                                                                                     121 GGGATAGCCCCAGGAGAAATGGAGTCCAAAGTGGAACAAGCGGTGAAAAATCTCAACATG 180
                                                                                                                                                                                                                                                                                                                                                  195 gaaaacgaagagetggageageecetgeagaatggacagaacacegeectgtgggagga 254
                                                                                                                                                                                                                                                                                                                                                                                             255 ggtgagggccaccagcctgctgcaaacaacaacaacaacaaccacaaccataaccacaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 caccaccgaagaggccaggctcgccgacctgccctaacttccgatgggccattcccaac 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 GGTCGCAGGCGGTTCCGGCTTCGCCAGCCCATCGTGCACTACAGATGGGACCTGATGCAT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 aggcagatgaatgacgggttgggtggagatggagatgatatggaaatgttcatggaggag 434
           299755.1 GI:3036782
HTG: COX7B; cytochrome c oxidase.
human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                555 eggteatteecectgagat 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  532 CTGAGCTTTTTCTGAAGAT 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lomo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
HS714B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
```

repeat_region repeat_region

```
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 45678)
Whiteley,M.
Direct Submission
Direct Submission
Direct Submission
Submitted (09-APP-1995) Sangér Centre, Hinxton, Cambridgeshire,
CB10 1RQ, UK. E-mail enquires: humquery@sanger.ac.uk
IMPORTANT: This sequence las the entire insert of clone V351P8. The Frue left and of clone V351P8 is at 1 in this sequence. The true
right end of clone V351P8 is at 45678.
V351P8 is from the human chromosome X-specific cosmid library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /partial
/porte='Alu repeat: matches 80. .1 of consensus'
642. 930
/hote='Alu repeat: matches 1. .308 of consensus'
1406. .5179
/note='Li_element fragment'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 // Apple 13.0 / Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Alu repeat: matches 308, .1 of consensus"
14478, .14650
/note="THEIB element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Alu repeat: matches 308. .1 of consensus"
19420. .19449.
/note="15 copies of 2 mer 87 % conserved"
complement(19537. .20013)
/note="match: 3' EST NS1315 clone 283089*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="17 copies of 2 mer 82 % conserved"
$279. .5567
Peartial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   // 1999. .15533
//note="11 element fragment"
|5534. .15626
| 15639 of 3 mer 85 % conserved"
|5566. .15639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="22 copies of 2 mer 98 % conserved" 20073. 20112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16352, 16436
Motea-11 element fragment*
16728, 16763
Anotea-9 coptes of 4 mer 94 % conserved*
16764, 17054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="3 copies of 18 mer 98 % conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ). .ii840
:="MLTIR element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e-"THEIB element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...vce-"L1 element fragment" 5243. 5276 5276 5277 5276 5279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91. 14536 Lement fragment te-"MSTA element fragment" 15. 14831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12437. 12502
/note="MSTC element fragment"
12756. 13059
                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="X"
/clone="GRC-351F8"
/clone="GRC-351F8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                       REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prepared with primer pairs provided by Sandoz, derived from N51315
- Washington University Merck EST sequence.
1 . 477
/ Organism-Homo saplens
4 . 467
- 44 . 467
- 44 . 67
- bind 44 . 67
- bind complement (130 . 149)
153 a . 115 c . 79 9 . 130 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSV351F8 45678 bp DNA PRI 23-NOV-1999
Human DNA sequence from cosmid V351F8, between markers DXS366 and DXS87 on chromosome X contains ESTs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 14.5%; Score 101.4; DB 11; Length 477; Best Local Similarity 72:9%; Pred. No. 4.5s-16; Indels 9; Gaps Matches 101; Conservative 0; Mismatches 51; Indels 9; Gaps
                                                                                                                                                                                                                                                                                                                                  94 degrees C for 15 seconds
60 degrees C for 30 seconds
72 degrees C for 23 seconds
30
Perkin Elmer 9600
                                                                                                                           Primer B: AMCATCTTCCATGAAACTTGATG
Primer B: CTTTTGGCATTCTTGGAA
STS size: 106
PCR Profile:
Initial incubation: 95 degrees C for 10 minutes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 ng
Primer: 25 ng
Primer: each 1 uM
dWTPs: each 200 uM
Amplifrag Gold Polymerase: 0.7 units/ul
Foral Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         513 caccacgatcaccatgatgaattctgccttatgccttgact 553 [1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 
    Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.5 mM
50 mM
10 mM
8.3
                                                                                                                                                                                                                                                                                                                                  Denaturation:
Annealing:
Polymerization:
PCR Cycles:
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270719
270719.1 GI:1261915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MgC12:
KC1:
Tris-HC1:
pH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buffer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STS
primer_bind
primer_bind
primer_bind
BASE COUNT
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
HSV351F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
```

δ

õ

δλ

us-09-327-750d-28.rge

0y 380 gatgalgacgggttgggtggagttggagtgatetggaatttcatggaggagtgg 439	RESULT 14 H6535G19 H5635G19 H5635G19 H5635G19 H5635G19 H5635G19 H5635G19 DEPINITION Human DNA sequence from clone 635G19 on chromosome 7422.1.22.3 Contains a LAMR1 (Laminin Receptor 1 (67kp) (408 Ribosoma) Fortein 5A, P40)) pseudogene and part of a novel protein. Contains ESTS and GSSs, complete sequence. VRRSION AL035494 VRRSION AL035494 VRRSION AL035494 VRRSION FIG. 406 Ribosomal Protein P40, 408 Ribosomal Protein SA; CpG SURCE human.	N NONZ F	rogether with a note of the overlapping clone mane. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers agiven in the feature table with their source databases: Em.; EMBL; Sw.; SWISSEROY; Tr.; TREMBL This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' facture & Key. This sequence is ambiguous, there is an annotation using the 'unsure' facture & Key.	Muman chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/EGP/ChrX
Db 256 AGGAGGGGAGCACCACACGAATGAAGAATATCCCGCCATTTGGGAGGGGGTGA 315 260 999ccaccaCGCCCCCCCCACGCAATGAAGAACAATCCCGCCATTTGGGAGGGGGTGA 315 260 999ccaccaCGCTGCAGAAATATCA	U + U	AX10031 AX10031 AX10031 AX100331 AX100331 GI:13539115 human. M Homo saplens Eukaryota, Metazoa, Chordata, Mammalia, Eutharyota, Metazoa, Chordata, Azing, Y. Y., Hillman, J. L., Yue, F. Azing, Y. Y., Hillman, J. L., Yue, Parterson, C.	.iation 31. 5; Length 1364;	Matches 269: Conservative 0; Mismatches 153; Indels 57; Gaps 4; 0y 143 geccagatageaecaggaaccaartcatcatggceafgccaectgccaccaggaacacgg 202 0 14 11 1 11 <

ζ

à

ò

o,

```
Query Match 11.1%; Score 77.4; DB 11; Length 244; Best Local Similarity 90.2%; Pred. No. 9.6-10; O. Matches 10; Conservative 0; Manches 21; Indels 5;
30
Perkin Elmer 9600
                                        Template: 25 ng
Primer: each 1 uM
MYNPS: each 200 uM
Tag Polymerase: 0.05 units/ul
Total Vol:
                                                                                                                                                    2.5 mM
50 mM
20 mM
8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: March 11, 2002, 16:33:03
Job time: 8158 sec
  PCR Cycles:
Thermal Cycler:
                                          Template:
Primer:
dNTPs:
                                                                                                                                                                            Tris-HCl:
pH:
                                                                                                                                                    MgC12:
KC1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protocol:
                                                                                                                                        Buffer:
                                                                                                                                                                                                                                                                                          STS
primer_bind
primer_bind
BASE COUNT 5
                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens

Bukaryotes, Metazoa; Chordata;

Bukaryotes, Metazoa; Chordata;

Waterbotas, Gathostomata, Osteichtiyes; Sarcopterygil; Choanata;

Tetrapoda; Anniota; Mammalla; Theria; Butheria; Archonta; Primates;

Catarrhini; Hominidae; Homo.

1 (bases 1 to 244)

Whyerbars R.M.

Unpublished (1995)
                                                                                         Db 64358-AGGAGGAGGAGCCCCCACAAAAGAAGAAGAAACCCGCCATTGGGAGGGGGGTGA 6417
                                                                                                                                                                                                                                   Oy 320 ccgaagaggcaaggtcgcgacctgccctaacttccgatgggccattcccaacaggca 379

bb 64444 --GcGGGGGGGTAAGCCACTTGTCCCTAATTTCGATGGGCATACTAAGGA 64501
                                                                                                                                                                                                                                                                                                                                                         Db 64502 TATTGAGCACAA-----TGAAGCGAGAGATGATGAGAAGGTTTGTAGGGCAGATGAT 64555
                                                                                                                                                                                                                                                                                                                                                                                                                      203 agagetggageag---cecetgeagaatggaeaggaacecegeeetgtgggaggaggtga 259
                                                                                                                                                                                                                 380 gatgaatgacgggttgggtggagatggagatgatatggaaatgttcatggaggagatgag 439
                                                                                                                                                                                                                                                                                                                                                                                                Oy 440 agagateeggagaaagettagggagetacagetgagaaattgtetacgeateettatggg 499
                            Ouery Match 11.5%, Score 80.2; DB 9; Length 69648; Best Local Similarity 56.2%, Pred. No. 2.4e-10. Matches 269; Conservative 0; Mismatches 159; Indels 57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        560 attocccctgagatccatactgtgactcccgctgtagccctttccctcgcattttcct 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 degrees C for 15 seconds
62 degrees C for 23 seconds
72 degrees C for 30 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Richard M. Myers
Stanford Human deenome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259689
Email: myerséshgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G13550.1 GI:1129289
STS sequence; primer; sequence tagged site.
human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer A: CCGTTTGCTGTACCCTAT.
Primer B: TTTAAATTTTTCCATGCAAATGG
STS size: 138
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Denaturation:
Annealing:
Polymerization:
repeat_region 27976. .28273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G13550 244 bp
human STS SHGC-11140.
G13550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
G13550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
JOURNAL
COMMENT
```

us-09-327-750d-28.rst

```
2 (bases I to 809)
I to Roberto, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itch, M., Komo, H., Okezaki, Y., Muramtsu, M. and Rayashaki, Y.
Romalization and subtraction of cap-trapper selected chikat, Y.
Genome research. 110 (10), 1617-1630 (2000)
BPL66996 00175392
BIZ49717 602996190
AA215070 mu76f04.7
AA066573 velee06.1
AA06017 mu77461.11
AA06017 mu77461.11
AA06017 mu77461.11
AA06017 mu77461.11
AA06019 mu77461.11
AA06019 mu77461.11
AA06019 mu77461.11
AA06019 mu77461.11
AA0605 mu77469.11
AA0606 u72590.1
AA0606 u72590.1
AA0606 u72590.1
AA0606 u72690.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3. (bases 1 to 809)
Shibata,K., Itch,M., Alzawa,K., Nagacka,S., Sasaki,N., Carninci,P., Konno, H., Akiyama,J., Vishi,K., Kitsunai,T., Tashiro,H., Itch,M., Konno,H., Akiyama,J., Vishi,K., Katsunai,T., Tashiro,H., Harada,A., Yamanotch,R., Akamurco,B., Saksquchi,S., Ikashiwaj,K., Yamanotch,R., Andrawa,Y., Izawa,M., Ohara,E., Watchiki,M., Yoneda,Y., Ishikawa,T., Cawa,K., Tanaka,T., Matsurra,S., Kawai,J., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsurra,S., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryote, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 809)
Cerninot, P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning Methods in ensymology. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKO04531 809 bp mRNA HTC 05-JUL-2001 Mus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone:1190011J73, full insert sequence. AKO04531. 1 GI:12835760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAP trapper.

Managed and action (Strain C57BL/6J) 18 days embryo CDNA to mRNA, clone_11b:RIKEN full-length enriched mouse cDNA library clone_11b:RIKEN full-length enriched mouse cDNA library and menschlugg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
       RESULT 1
AKO04531
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
          AKO04511 Mus muscu
AKO1050 Mus muscu
BE608455 MTL_00139
AT110890 ue93-608.7
AA77466 ue76402.7
AA772375 vb62407.7
AA772375 vb62407.7
AA772375 wms umscu
BE334877 us90b10.7
BE334877 us90b10.8
BE334867 us90b10.8
                                                                                                                                                                                            March 11, 2002, 13:08:25; Search time 1609.39 Seconds
(Hithout alignments)
(4673.848 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.
                                                                                                                                                                                                                                                                                                      US-09-327-750D-28
1 00
1 a oyaqcqtctggccagcaqcaqc......ggggcttgtgttgccagtga 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22703874
                                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 00%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  em_estin:
em_estin:
em_estin:
em_estin:
em_estin:
em_estin:
em_estin:
em_estin:
em_ts:
em_ts:
em_ts:
em_tss:
e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2: em_estfun:

2: em_estfun:

4: em_estfn:

4: em_estpl:

6: em_estpl:

6: em_estpl:

6: em_estpl:

7: em_estro:

8: em_estro:

8: em_estro:

8: em_estro:

10: 9D_estro:

11: 9D_estro:

12: 9D_htc:

13: 9D_estro:

14: em_gss_tun:

15: em_gss_tun:

16: em_gss_tun:

17: em_gss_tun:

18: em_gss_tun:

19: em_gss_tun:

19: em_gss_tun:

10: em_gss_tun:

11: em_gss_tun:

11: em_gss_tun:

12: em_gss_tun:

13: em_gss_tun:

14: em_gss_tun:

15: em_gss_tun:

16: em_gss_tun:

17: em_gss_tun:

18: em_gss_tun:

19: em_gss_tun:

11: em_gss_tun:

11: em_gss_tun:

12: em_gss_tun:

13: em_gss_tun:

14: em_gss_tun:

15: em_gss_tun:

16: em_gss_tun:

17: em_gss_tun:

17: em_gss_tun:

18: em_gss_tun:

18: em_gss_tun:

18: em_gss_tun:

19: em_gss_tun:

19: em_gss_tun:

10: em_gss_tun:

10: em_gss_tun:

11: em_gss_tun:

11: em_gss_tun:

12: em_gss_tun:

13: em_gss_tun:

14: em_gss_tun:

15: em_gss_tun:

16: em_gss_tun:

17: em_gss_tun:

18: em_gss_tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Cuery
Guery
Guery
Guery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST:
                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        687.4
687.4
637.6
627.6
606.8
591.4
585.4
585.4
556.6
535.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
No.
```

```
/codon_start=1
/protein_id="Bha56986.1"
/protein_id="Bha56986.1"
/db_xref="61:12845992"
/translation="ManwHQENEEMEOPLODGOEDRPVGGGEGHQPAANNNNHHHN
HWHRRGCARRA-PRERALIENGOMDGLGGDGDDMEMFWEEMREIRRERELGLENC
HHRHRGCARRA-PRERALIENGES
HHGELSHHPHHPEFCLAMP
629...834
//note="putative"
845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 01-APR-2001
ICRFp522 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 gictacgcatccttatgggggggcgtctaaccaccacgatcaccatgatgaattctgcc 540
482 grchaccarcctparggaggggagctgrctaaccaccacgatcaccatgatgaattctgcc 541
482 grchaccarcctparggaggaggcrgrctaAccaccaccarcaccarcaccarcaccaccaccaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 ttatgccttgacttcggtcattccccctgagatccatactgtgactcccgctgtagccc 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

Query Match

98.2%; Score 687.4; DB 12; Length 845;
Best Local Similarity 99.1%; Preced. No. 2.44-152;

Marches 691; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF608455 787 bp mRNA EST
MYI_001397 Mouse 9-day fetus CDNA library IC
CDNA clone ICRF6522N0111 5', mRNA sequence.
BF608455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttccatgccatgtgcaggtggggttgtgtgtgcag 697
                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"putative"
226 a 215 c 231 g
                                                                                                                                                                                                                                                                                     polyA_signal
                                                                                                                                                                                                                                                                                                                                                                            polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
BF608455
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 6 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 6 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 % a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o de o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adachi, A. Alacada, A. Akahira, S., Akimura, T., Aono, H., Arai, A., Akahira, S., Fakuda, S., Manda, S., Kauda, S., Kurihara, C., Mateuyama, T., Kojima, Y., Konoh, H., Kouda, M., Koya, S., Kurihara, C., Mateuyama, T., Kojima, Y., Konoh, H., Kowa, S., Kurihara, C., Mateuyama, T., Kojima, Y., Konoh, M., Kako, M., Kato, H., Kato, M., Kato, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Genere and Genome Sciences Activation of Experimental Animal Research in Riken contributed to Division of Experimental Animal Research in Riken contributed to Division of Experimental Animal Research in Riken contributed to Prepared by using trehalose thermo-activated Teveres transcriptuse and subsequently enriched for full-length by cap-trapper. ODNA west through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand CDNA was prepared with the primer adapter
                                                                                                                                                                                                                                                                                                                        11042199
2 (Abses 1 to 845)
2 (Abses 1 to 845)
5 (Ablata, K., Itoh, M., Alzawa, K., Ritsunai, T., Tashiro, H., Itoh, M.,
Konno, H., Akiyama, J., Wishi, K., Ettsunai, T., Tashiro, H., Itoh, M.,
Sumi, M., Ishi, Y., Nakamira, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakayuch, S., Ikegami, T., Kashiwaqi, K.,
Yoneda, Y., Ishikwa, T., Toswa, M., Ohara, E., Hatahiki, M.,
Yoneda, Y., Ishikwa, T., Ozwa, K., Tanaka, T., Matsuna, S., Kawi, J.,
Okazaki, Y., Minamatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
Genome casearch and Hayashizaki, Sequencing pipeline with 38 multicapillary sequencer
E Gorome research. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 185
1. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROL = 12.0. Second strand cDNA was prepared with the primer adapter of acquence lossesses of acquence 1. Second strandary and second se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 (bases 1 to 845)
FANTON CONSORTION Research Group Phase II Team and the FANTON CONSORTION.
FANTON CONSORTION.
Functional amortation of a full-length mouse cDNA collection Nature 409, 685-560 (2001)
     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Mormalization and subtraction of cap-trapper-selected CONAs to prepare full-length CDNA libraries for rapped discovery of new genome research. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                          JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
BFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
```

```
Tunor dear Index (1977)

Tunor dear Index (1977)

Daulished (1977)

Email: cgapber Strausberg, Ph.D.

Email: cgapber Strausherg, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center (Cone distribution NII-CGAP clone distribution information can be waw-blo.lln.gov/bbrp/lmage/lmage.html
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 tgcagaalggacaggaacacacacatggagagaagtgagggcaccacagcctgctgcam 279
181 TCACAAATGACAACACCGCCCTGTGGAACAACACACCTGTTGAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 ggaaacaaaatctcatcatggccaatgtccaccaggaaaacgaaggctggagcagccc 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 aceacaacaacaacaccacaaccataaccacaaccaccaccgeaqaggccaggctcgcc 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gggagctacagctgagaaattgtctacgcatccttatggggggagctgtctaaccaccacg 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 ggoggetggcocgaggcocgaggcgagcgggcagttgactgaagcogaggtccag 99 [III] [III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Watch

86.7%; Score 606.8; DB 10; Length 628; Bett Local Similarity 97:8%; Pred No. 25-133;

Marches 614; Conservative 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460
   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a à
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A4476468 628 bp mRNA EST 24-FEB-2000 sugfador.yl NCI-COAF_L133 Mus musculus cDRA clone IMAGE:2937027 5' stallar to 95:M98188 OVARIAN GRANUIOSA CELL 13:0 KD PROTEIN HGR74 A4476468.1 GI:7046574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 628) NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                              ccaatgiccaccaggaaaacgaagatggagcagccctgcagaatggacaggaacacc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 goootgigggaggaggtgagggccaccagootgotgcaaacaacaacaacaacaca 300
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                          41.5%b. Library constructed by Dr. Sumio Sugano (indiversity of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer crycyccyclaAnGCTSCG and 3' end primer archivestochackacka. It is 17, c 181 g 111 t 2 others
                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                   Query Match

89.74; Score 627.6; DB 10; Length 642;
Best Local Similarity 99.14; Pred. No. 3.1e-138;
Matches 630; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
Mus musculus
                                                                                                                     171 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
AW476468
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247
```

d y

ŏ g ŏ 8 6 8

6 6 6

8 6 6 6 6

6 6 6

g ò

ö

Gaps

```
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itob, M., Konno, H., Okazaki, Y., Muranatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected CDMAs to
prepare full-langth CDMA libralisa for raple for the Conner research. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shibates 1 to 826)
Shibates X. 1tob, W. Alzava, K., Nagaoka, S., Sasaki, N., Carninci, P., Shibate, X. 1tob, M., Alzava, K., Kiteunai, T., Tashiro, H., Itob, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Tamamoto, R., Matsumoto, H., Sakauchi, S., Itegani, T., Kashwaqi, K., Vonamoto, R., Mitsumoto, H., Sakauchi, S., Itegani, T., Kashwaqi, K., Vonamoto, R., Mitsuma, M., Tana, M., Ohara, E., Hatahiki, M., Vonada, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, H., Inoue, Y., Kira, A. and Hayshizaki, Y. Rikki Niegrated sequence analysis (RISA) system-384-format Genome research. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Summission of the Submitted (16.70L-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Vokohama Institute; 1-7-22 Submitths-Choup, Taurumi ku, Yokohama, Ranagawa 230-0045, Japan (E-mali;genome-reseggac.riken.go.jp, OR::181-45-503-9212), Phiesse visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             usu misturian Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (basea 1 to 826)
Erachinci, P. and Hayashtaski, Y.
High-efficiency full-length con
                                                                       AK003294 B26 bp mRNA MISTERN full-length enriched hus musculus 18 days embryo cDNA, RIKEN full-length enriched library, clone.1110002F04, full insert sequence.
AK003294, I GI:12833872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAP trapper.

Mus musculus (strain:057BL/63) 18 days embryo cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:1110002F04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         irect Sub
ubmitted
hysical a
                                                                                                                                                                                                                                              RESULT 8
AK003294
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                       ç
                                                                                                                                                                                                                                                                                                                                                                                                                                        1. G12

//Crganism="Mass musculus"
//Crganism="Mass musculus"
//Strahi="FVBAN"
//db_xref="taxon:10000"
//clone="limAdB:761618"
//clone="limAdB:761618"
//clone="limAdB:761618"
//clone="limAdB:761618"
//clone="limAdB:761618"
//clone="limAdB:761618"
//clone="limAdB:761618"
//clone="cryon="limade"
//tissue_rype="pooled organs"
//clone="cryon="limade"
//clone="cryon="cooled organs"
//clone="cryon="cooled organs"
//clone="cryon="cooled organs"
//clone="cryon="cooled organs"
//clone="cryon="cooled organs"
//clone="cooled organs"
//clon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
Washlu-HHMI Mouse EST Project
Washlugton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 134 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 114 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 agattgactggaagcogagagtccaggcggcagcgggaattgacaggagactacgccgc 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caggcagatgaatgacgggttgggtggagatgagagatgatatggaaatgttcatggagga 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 gatgagagagatccggagaaagcttagggagctacagctgagaaattgtctacgcatcct 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 84.3%, Score 590.4; DB 10; Length 612; Best Local Similarity 99.0%, Pred. No. 1.9e-129; Matches 594; Conservative 0; Mismatches 6; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 507. Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374
                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
```

à q ò

8 8 8

Tue Mar 12 09:01:24 2002

```
/orgalism=*Mus musculus*
/orgalism=*Mus musculus*
/orgalism=*Musculus*
/clone_llb=*Soares_mammary_gland_NMLMG*
/clone_llb=*Soares_mammary_gland_NMLMG*
/itssue_type="nammary gland"
/lab_nost=*PH10B*
/lab_nost=*PH10B*
/lab_nost=*PH10B*
polylinker; lst strand cDNA was prepared from mammary
gland tissue from a lactating female_and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Ecc Rt adaptors (Pharmacla) digsted to the
modified pT/73 vector Library is normalized. Library
was constructed by selector clabrary is normalized.
1 prince of the Not I and Ecc Rt aleas of the
mass constructed by selector clabrary is normalized.
1 chers a constructed by selector clabrary is normalized.
IMAGE Consortium (info@image.llnl.gov) for further information. MGI:106979.
MGI:106979.
Seq primer: -40RP from Gibco
Seq primer: -40RP from Gibco
High quality sequence stop: 465.
Location/Qualitiers
1. .885.
                                                                                                                                                                                                                                                                                                                                                                                                                         gagatgagagatccggagaaagcttagggagctacagctgagaaattgtctacgcatc 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cttatgggggggctgtctaaccaccacgatcaccatgatgaattctgccttatgccttga 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          72 acagattgactggaagccgagagtccaggcggcagcgggaattgacaggaggactacgcc 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caggaaaacgaagagctggagcagccctgcagaatggacaggaacaccgccctgtggga 251
                                                                                                                                                                                                                                                                                                                                                            Match 81.7%; Score 571.6; DB 10; Length 565; Local Similarity 99.1%; Pred. No. 5.3e-125; Indels 0; Ss 574; Conservative 0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ďq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF178306
                                                                                                                                                                                                                                                              162
                                                                                                                                                                                                                                                                                                             Query Match
Best Local S:
Matches 574,
                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
BF178306
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492
                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE334877 585 bp mRNA EST 14-JUL-2000 190516. Sign bp mRNA EST 14-JUL-2000 1MAGE:335627 5' similar to gland_MNLAG Mus musculus CDNA clone LAMGE:335627 5' similar to gland. Sign bendili MRNA (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Egg.

Mus musculus

Mus musculus

Mus musculus

Musryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musryota: Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Musryota: Musculus

Musryota: Musculus

Musryota: Musculus

Musroal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Robert Strauberg, Ph.D.
Daali: cgapbs-refamilinhgov
This clone is available royalty-free through LLNL; contact the
                                                                                       ggacagattgactggaagccgagagtccaggcggcagcgggaattgacaggaggactacg 129
                                                                                                       130 ccgcaagggataggcccagaatagcaaccaggaaacaaaatctcatcatggccaatgtcc 189
                                                                                                                                                        190 accaggaaaacgaagagctggagcagccctgcagaatggacaggacacgccctgtgg 249
                                                                                                                                                                                                       310 acaaccaccaccaacgaagaccaggccagacctgccctaacttccgatggccattc 369
263 ACAACCACCACGAAGAGCCAGCCAGCCACTTGCCCTAACTTCCCATGGCCATTC 322
                                                                                                                                                                                                                                                                                                                                  tecttatgggggagetgtetaaccaccacgateaccatgatgaattetgeettatgeett 549
                                                                                                                                                                                                                                                                                                                                                                                                                                               gacticggtcattccccctgagatccatactgtgactccgctgtagcccttccctcg 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                 46;
                Indels
    Best Local Similarity 92.6%; Pred. No. 1.7e-126; Matches 637; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atgtgccaggtgggcttgtgttgccag 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                       443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
BE334877
                                                                                                            a
                                                                                                                                                                                                       8 6 6
                                                               셤
                                                                                      à
                                                                                                                                 S B S
```

ö

```
/db_xref-"taxon:10090"
/clone-"IMAGE:4017071"
/clone-IMAGE:4017071"
/clone-IMD-"4017071"
/tissue_type-"spontaneous tumor, metastatic to mammary.
Stem cell orligin
/tab_host-"bH108"
/note-"07gan: Lung; Vector: pcwv-sporr6; Site_1: Sali;
/note-"07gan: Lung; Vector: pcwv-sporr6; Site_2: Not; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Like Technologies. Investigator
providing samples: Gilbert Smith, NiH"
205 c 208 g 162 t
                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B1249717 918 bp mRNA EST 17-JUL-2001
602996190F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5151719 5',
mRNA sequence.
B1249717
                                                                                                                                                                                                                                                                       417 gazatgitcaiggaggagatgagagagatccggagaaagcitagggagctacagctgaga 476
                                                                                                                                                                          Query Match 76.2%; Score 533.2; DB 11; Length 810; Best Local Similarity 95.5%; Pred: No. 6.7e-116; Matches 615; Conservative 0; Mismatches 18; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI249717.1 GI:14797369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
Mus musculus
                                                                                                                              235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
B1249717
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                            ç
                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                        $ a 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oy
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is EST.

house mouse.

ISM Mus maccilus

Enkaryota. Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Enkaryota. Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammala, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(CE 1 (base) 1 to 610)

NS NIH-MacChtp.//mac.ncl.nih.gov/.

SR NIH-MacChtp.//mac.ncl.nih.gov/.

NAL Unpublished (1999)

Tontaci: Robert Straubsery Ph.D.

Emali: Gapba-Frequation: Life Techhologies, Inc.

CDNA Library Arrayed by: The I M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

CDNA Library Arrayed by: The I M.A.G.E. Consortium/LINL at:

CDNA Library Arrayed by: The I M.A.G.E. Consortium/LINL at:

High quality sequence stern: 3

High quality sequence stern: 2

High quality sequence step: 659.

Locatic Library Arrayed by: 559.

High quality sequence step: 659.

High quality sequence step: 659.

Locatic Library Arrayed maccilus*

1. R100

Normanism-*Mus musculus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIGG928 810 bp mRNA EST 30-OCT-2000 (60175392F1 NCL_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017071 5', MRNA Sequence. BF168928 (6111049280
                                                                                                     61 ACAGATTGACTGGAAGCCGAGAGTCCAGGCGGCAGCGGGAATTGACAGGAGGAGATTAGCTACGCC 120
                                                                                                                                                                                                      ggaggtgagggccaccagcctgctgcaaacaacaacaacaacaaccacaaccataaccac
                                                       72 acagattgactggaagccgagagtccaggcggcagcgggaattgacaggagtactacgcc 131
        552 ct 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
BF168928
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                      252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
```

666666

ŏ

8 6 8 6 8

Search completed: March 11, 2002, 16:09:50 Job time: 10885 sec

6.33.03 ; Search time 1319.57 Seconds 6.33.03 ; Search time 1319.22 Million cell updates/sec 6.33.03 ; Search time 1319.22 Million cell updates/sec 6.33.03 ; Search time 1319.22 Million cell updates/sec 7.26.4 277. 24.4	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	Query Match Length DB	Description M38188 Human unkno
Content Cont	*	609.4 68.4 793 9	AF187064 Homo sapi BC003190 Homo sapi
186 187		5 354.2 39.8 421 11.0 6 312.2 35.0 700 10 7 254.4 29.7 519 10	G72708 MARC 4953-4 G72708 MARC 4953-4 AF187066 Mus muscu AF18706 Rattus no
1112 115		242.4 27.2 562/4 9 242.4 27.2 244 11 185.2 20.8 45678 9 158.6 17.8 69648 9	(13550 human STS E 270719 Human DNA 9 AL035494 Human DNA 9 AL035494 Human DNA 9 AL000659 Human DNA
1.2 1.2		13 141.2 15.8 1364 6 141.2 15.8 43952 9	AX100231 Sequence Z92846 Human DNA S
11 11 11 11 11 11 11 1		15 132.4 14.9 477 11 16 122.2 13.7 35714 9	ALOO8708 Human DNA
20 110 6 12.4 4 112.2 9 183977018 20 110 8 12.4 4 112.2 9 183977018 21 100 8 12.3 4 1054 9 12.3 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054 9 12.3 4 1054	parameters:	18 117.2 13.2 154959 2	AC009282 Homo sapi
24 109.8 12.3 4084 9 AR21048 2 AR21048 2 AR21048 2 AR21048 3 AR2108 3 AR2104 11.7 7 84 9 AR210103	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	110.8 12.4 31321 9	ALO22169 Human. DNA S ALO22169 Homo sapi
Color	Post-processing: Minimum Match 08 Maximum Match 100* Listing first 45 summaries	22 109,8 12,3 642 9 24 109,2 12,3 40584 9 25 108,2 12,1 791 9	AF103410 HOMO SAPI AF220189 HOMO SAPI AL133348 HUMAN DNA AF237783 HOMO SAPI
SHOHEDE	Genbbl:* Genbbl:* 9D_htg:* 9D_no:* 9D_oo:* 9D_oo:*	d auchidologoppe popolog	### ##################################
	SUMMARIES	COMMENT Draft entry and computer-readable sequence for [DNA 9, 479-485 (1990)] kindly submitted	for [DNA 9, 479-485

	USA NIH-WGC Project UKL: http://mgc.ncl.nih.gov Contect: MGC help desk Contect: MGC help desk Tissue Procurement: ATC Tissue Procurement: ATC CDN Library Preparation: Rubin Laboratory CDN Library Preparation: Rubin Laboratory CDN Attayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Genome Sequence Centre.	DC Concer Agency, Vancouver, BC, Canada Info@concer, Dc, Canada Info@concer, Dc, Canada Steven Jones, Bennifer Asano, Ian Bosder, Yaron Butterfield, Steven Jones, Bennifer Asano, Ian Bosder, Yaron Butterfield, Letticia, Read Mana, Chill, Chils Rela Russche, Oliver Lee, Sco Sen Lee, Victor Ling, Carrie Markerson, Canadice McLaewy, Steven Ness, Pawan Pandoh, Anna-Lilaa Prabhu, Parvanah Sacedi, Jacqualine	Michael Thorne, Mitranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Luyderduyn, Marco Marro. Clone distribution: MGC clone distribution information can be found through the I.M.A.G. Consortlum/LML at: http://maga.lnl.gov Series: IRM.Pates: 6 Row: K Column: 2 This clone was selected for full length sequencing because it.		/AD_XXEI=-EAXONI-9505 /clone="MGC:002 IMAGE:3357965" /tissue_type="Eye, retinoblastoma" /zhome_lib="NH# AGC_16"	/note-"Vector: porB?" 196. 531 /codon_start=1 /product-"P75NTR-associated cell death executor; ovarian	grantusa ceil proein (13xu)/ /protein_le—Aahd31901. /db_xref="G1:13112031" /tb_xref="G1:3112031" /translation="wantigemereRepowgneEnriceGergopaGarrad /translation="wantigemereRepowgneEnriceGergopaGarrad pwrgwa.rangolnowaGobodbeIrweEnriceGergopaGarrad	Similar	Sababasababat Charcat Garat Carca garat Carca garat 340 Sababa ababa Garat Carca Garat Car	341 gatgagcagcctatgcagaatggagagaagaccgccctttgggaggagggaaggca 400 [461 catecoatageagateatgatgatgggtggtggatgggatgggat
REFERENCE AUTHORS TITLE JOURNAL	REMARK COMMENT			FEATURES SOULCE		CDS		BASE COUNT ORIGIN OWERY MATCH BEST LOCAL	Oy 281 Db 165	9y 341 Db 225 Oy 401 Db 285	Oy 461 Db 345
	121 121 121 181	24) attegetetetetetetetetetetetetetetetegeteteaagaaaacaaccagaaaaa	301 AMAILTIANITATIOGAMAINTIANAMANAMANAMANAMANAMANAMANAMANAMANAMANA	421 481 481	<pre>Qy 541 tcagaagaacttagggagtgcagttgagtagtattgtctgcgtatccttatgggggagc 600 </pre>	601 tetetaateaceatgacateatgatgattttgeettatgeettegaeteetgoattta 	bol rostopateraterograficosograficoru 	721 781 781	D 841 TTCACCCATTGCATGGAAAATTTAAAGCTAATAAAGCAATTTAAAAAGC 891	REBULT 3 BC001190 LCCUS BC001190 T93 bp mRNA DFINITION Homo sapiens, p78NF-associated cell death executor; ovarian granulosa cell protein (13kD), clone MGC:802 IMAGE:3357965, mRNA, ACCESSION BC003190 NERSION BC003190.1 GI:13112030	SOURCE human. ORGANISM Homo sapiens ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
2. (bases 1 to 70).
Hundly, Hothiya,T., Hoshino,S., Kimura,M., Nadano,D., Suvanto,P., Hundly,T., Hachiya,T., Irie,S. and Sato,T.

Direct Submission.

Direct Submissio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (Abasa 1 to 70), Shoji-Hoshino, S., Kimura, M.T., Nadano, D.,
Mukil, J., Hansonskar, L. Lif, Irie, G., Greener, L.A. and Sato, T.A.
NADE, a pishrrassociated cell death executor, is involved in
signal transduction mediated by the common neurotrophin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                              AF187066 700 bp mRNA ROD 11-JUH-2000 mRNA.

Made) mRNA.
complete cds.
AF187066 1 G1:8452897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 amanchanchagamananantotohtohtogramatattohooggamangagat 343
119 ATAKOHACHAGAACHAATCTOROKTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOTOHOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOGHITOOOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404 gcctgcaggaa-----atcgacgggg 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     425 acaggetegecegaetegecectaatttegatgggecatacecaataggeagateaatga 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 35.0%, Score 312.2; DB 10; Length 700; Best Local Similarity 78.5%; Pred. No. 1.7e-75; Indels 45; Gaps Matches 431; Conservative 0; Mismatches 77; Indels 45; Gaps
121 CCTGATATGCCTTTACTGATCCATTTGCTGTGAACCTTATGTAATTTCCATGTGTCAGGT 62
                                                                                    J. Biol. Chem. 275 (23), 17566-17570 (2000)
20298829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.700

Organism. Mus musculus.

/strain. Pale/c.

/db_xref_taxon:10090.

1.700

1.700

1.707.551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                RESULT 6
AF187066
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ογ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The STS is derived from PCR amplicons generated from genomic DNA, sequence drom each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was triamed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next 10 bases averaged a quality score of cor greater. Amplicon size was estimated by agarcse gel electrophoresis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cctaatatgcctttactgatccgtttgctgtgaacctatgttatttccatgtgtcaagt 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 aatogacgggacaggctcgccgattgcccctaatttcgatggccaacccaatag 473 [http://www.new.cccaatag 473 antakacgacaaracccaatag 473 antakacgacaaracccacgaccaaraccccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaraccaaracc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / organism-Sus scrofa*
/organism-Sus scrofa*
/organism-Sus scrofa*
/organism-Sus scrofa*
/ob_xrefa-rexon:9823*
/sex-male and female*
/olone_lib-"SCF porcine spleen*
/dev_stage="adult"
/note-"Organ: spleen*
/olone_lib-"SCF 86 g 102 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 39.8%, Score 354.2; DB 11; Length 421; Best Local Similarity 92.1%, Precd. No. 38-87; Matches 33, Matches 384; Conservative 1; Mismatches 29; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Template: 50-200 ng genomic DNA Primer: each 20 pmoles each 88 uM GMPPs: Pag-Polymerase: 0.25 units (Qlagen HotStar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Commercially supplied Qiagen HotStar buffer
            Contact: Freking BA
USDA, ARS, US Weat Animal Research Center
DO BOX 166, Clay Center, NE 6993-0166, USA
Tel: 402 762 427 Center
Email: freking Gemail.marc.usda.gov
Primer A: GCAAATGGGTGAAACTTACT
Primer B: CCAGCGAAATAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hoistart: 95 degrees for 15 minutes Dennure: 95 degrees for 30 seconds Anneal: 65 degrees for 2 minutes Excension: 68 degrees for 2 minutes Cycles: 32 to 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protoco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buffer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STS
BASE COUNT
ORIGIN
```

ë,

Ş 2

ò do y

a O O

ò

ð

```
/note-'Alux' repeat: matches 34. .295 of consensus' /note-'Niu' repeat: matches 67. .212 of consensus' /note-'Alux repeat: matches 67. .212 of consensus' /note-'Alux repeat: matches 1. .300 of consensus' /note-'Min repeat: matches 82. .262 of consensus' /note-'Min repeat: matches 82. .262 of consensus' /note-'Libbl repeat: matches 5970. .6224 of consensus' /note-'Libbl repeat: matches 5970. .6224 of consensus' /note-'Aluxgi repeat: matches 1. .303 of consensus' /note-'Aluxgi repeat: matches 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       //orde="LiM2 repeat: matches 1776. 1898 of consensus" 21212. 21391 repeat: matches 1776. 1898 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       te-"HERVI6 repeat: matches 378. .650 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24456. .24590

14871. .24916

700ce-MIR repeat: matches 102. .143 of consensus*

25378. .25556

700ce-T2 repeat: matches 2330. .2519 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .... or consensus"
27040. 27107
27040. 27107
2708-12 repeat: matches 2572. 2649 of consensus"
27108. 27109. 27108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 36. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 repeat: matches 2330. .2519 of consensus*
25910
                                                                           18657. 18871
Note—"MIR repeat: matches 35. .252 of consensus"
18927. 19330
19492. .19559
19492. .19559
Note—"Mir repeat: matches 2. .67 of consensus"
19560. .19821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 1. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 1. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AluY repeat: matches 41. .304 of consensus" 27471
                                                                                                                                                                                                                                                                                                           00te-*MIR repeat: matches 48. .191 of consensus*
1/0944. .16040
//note-*WIR repeat: matches 102. .144 of consensus*
16116. .16184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15673. .35910
Mote-"Mir repeat: matches 4. .255 of consensus"
2672. .26798
/note-"L_repeat: matches 2572. .2649 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16116. 16184
/note="MERSS repeat: matches 3. .70 of consensus"
16897. .17005
               if repeat: matches 1. .300 of consensus"
3495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R repeat: matches 3, .86 of consensus"
2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23919. .24194
/note="AluSx re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note-"AluSq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /1392. .21.
/note-"MIR
           repeat_region
                                                                       repeat_region
                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                               misc_feature
Mapping Group. Further information can be found at http://www.sanger.ca.uk/MGPChir2 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variationas regenter with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. We we submit sequences with the following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Emm. EMBL, SW, SWISSPROT, Tr., TREEBL, Wp., WORMERP, Information on the WORWERP database can be found at
                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep CTA-714B7 1s from the human RAC library described in U-J. Kim et al. (1996) Genomics 44, 213-218.
VECTOR: pBeloEnds.
This sequence is the entire insert of clone CTA-714B7.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5. .5486
te-"LIMEc repeat: matches 2052. .2207 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258
te-"LINC5 repeat: matches 7840, 7913 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and the state of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-lime arrange 1538 of consensus" /note-"LIMD repeat: matches -1. .1538 of consensus" /note-"LIMD repeat: matches -1. .1538 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 2693. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6896. 7185

// note=-2.2 repeat: matches 2356. 2710 of consensus*

complement(7187. 7611)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-7. invaro
4-7. invaro
29. incompant: matches 1. .294 of consensus 29. .10563

    17594
    ote-"MIR repeat: matches 34. ,256 of consensus" uplement(7713. ,8092)
    ote-"match: GSS: Em:AQ071449"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 20. .95 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_10-*CTA_714B7*
/clone_110-*CIT978SK-A2*
109, .136
/note="14 copies 2 mer ac 100 conserved"
183, .258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Le-"match: GSS: Em:AQ566001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atch: GSS: Em:AQ284832"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch: GSS: Em: A0373724"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo saplens"
/db_xref="taxon:9606"
/chromosome="22"
/map="q12.2-13.2"
/clone="cra-71487"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86. .8300
ote-"MIR re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   //...1446
/note-"match.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18. .9890
ste="match
135. .1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1301. .1356
/note="L2 r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
```

```
Gaps
                         /note-niu repeat: matches 1. .260 of consensus 35804. .35839
//note-mills copies of 2 mer 83 % conserved 38625. .38705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
20.84; Score 185.2; DB 9; Length 45678;
Best Local Similarity 64.48; Pred No. 5.26-40;
Matches 345; Conservative 0; Mismatches 178; Indels 13;
                                                                                                                   /note-12 copies of 2 mer 98 % conserved."
/note-12 copies of 4 mer 100 % conserved."
20073...20126
20073...20126
20073...20126
20088...23300
20088...23300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: 5" EST H68599 clone 239077" comp.lement(32825...33280) //note="match: 3" EST H68239 clone 289077" 35551...3802
/note="9 copies of 4 mer 94 % conserved"
16764 .17054
                                                                                                                                                                                                                                            1318. 23489
note-"NLTIB element fragment"
3362. 23491
note-"MTIC_element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6284, .26343
note-"MLTID element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6428, .26491
note-"MLT1D element fragment"
6465, .26518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -"MLTIE element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"MLT1R element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Joseph Jacob
/note="MLTIE element fragment"
38965. 39076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-"MLTID element fragment"
9135 c 9327 g 12956 t
                                                                                                                                                                                                                               te-"MLTIA element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "MER25 element fragment"
                                                                                                                                                                                                                                                                                                                                                                   te-"MSTA element fragment"
                                                                                                                                                                                                                                                                                                                                                                                              "MSTA element fragment"
                                                                                                                                                                                                                                                                                                                                           C element fragment"
                                                                                                                                                                                                                                                                                                         .1 element fragment"
24462
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ote-"L1 element fragment"
439, .25696
                                                                                                                                                                                                                                                                                                                                                                                                                          note-"L1 element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7446. .27667
note="Ll element fragment"
8954. .29247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT 14260 a ORIGIN
                repeat_region
                                                       repeat_region
                                                                                                             repeat_region
                                                                                                                                       repeat_region
                                                                                                                                                                  repeat_region
                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                      HSV151PB 45678 bp DNA 1918, PRI 23-NOV-1999 Milman DNA sequence from cosmid V351PB, between markers DXS366 and DXS87 on Chromosome X contains SSTs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Alu repeat: matches 308. .1 of consensus" .14650
                                                                                                                                                                                                                                                                                                                                                                                                                         forte-*Alu repeat: matches 1, 308 of consensus*
forte-*Alu repeat: matches 1, 308 of consensus*
forte-*Alu repeat: matches 1, 308 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lu repeat: matches 304. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 copies of 2 mer 82 % conserved* 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   copies of 3 mer 85 % conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ies of 18 mer 98 % conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "MSTAR element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - "THEIBR element fragment". .11846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "MLTIR element fragment"
.12170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "THEIB element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5. .14831
b="THELB element fragment"
9. .15533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "MSTA element fragment"
12486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ="MSTA element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e-"MSTA element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISTC element fragment"
13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   element fragment*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               te="L1 element fragment"
13. 5276
hte="17 coples of 2 mer 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .ы element fragment"
.16763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "L1 element fragment"
. .15626
                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                    /clone="GHc-351F8"
/clone_lib="SCcV"
                                                                               70719.1 GI:1261915
                                                                                                             uman.
                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
 RESULT 10
HSV351F8
LOCUS
DEFINITION
                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                          ORGANISM
                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                    COMMENT
```

```
23735. .24041
/note-*Alusgal repeat: matches 1. .308 of consensus*
/note-*Alusgal repeat: matches 1. .308 of consensus*
24045. .24072
/note-*Alusb repeat: matches 1. .289 of consensus*
2583. .2544. .2542
/note-*HERVEL repeat: matches 23. .79 of consensus*
2614. .2646
/note-*HERVEL repeat: matches 13. .79 of consensus*
/note-*Alusb repeat: matches 13. .311 of consensus*
/note-*Alusb repeat: matches 13. .289 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="LIM4" | 27536. 27600 | /note="LIM4 | z 27601. 27975
                  repeat_region
                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                repeat_region
                                                                                                          repeat_region
                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D repeat: matches 4646. .5565 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20015, 20194

700-*MRX74A repeat: matches 295. .487 of consensus*

2034, .2069

20701. .20809
/note="LIMD repeat: matches 1357. .1972 of consensus"
11443. .11571
                                                                                                                                                                                                                                                                                                                                // Mote-15 copies 2 mer ct 77% conserved*
// Anote-15 copies 2 mer ct 77% conserved*
// Anote-1937/
// Anote-1939/
// Anote-19
                                                                                                                                ice-Mludb repeat: matches 136, .295 of consensus" 71, 16953 repeat: matches 126, .295 of consensus" te-Aluss repeat: ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="15" copies 2 mer at 79% conserved"
17704. 11863
1764. 11873
17864. 18175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       te-"MER74B repeat: matches 61. .368 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -"MER34 repeat: matches 409. .543 of consensus"
                                                      note-"FLAM. A repeat: matches 2. .129 of consensus" 1572. .1346
                                                                                                          repeat: matches 977. .1357 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acce-Min repeat: matches 92. .191 of consensus"
7016. .13198 cepeat: matches 1. .131 of consensus"
7018. .2308. .2004. 2 mer 476 conserved"
7016. .100ples 2 mer ta 768 conserved"
                                                                                                                                                                                                                                                                                        repeat: matches 177, .505 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5. 15909
e-*Alusx repeat: matches 24. .312 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       b4. .1817.77 te="Alurba repeat: matches 1. .318 of consensus" 76. .18298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 682. .785 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="LTR1 repeat: matches 1 . 195 of consensus" 21186 . 21536 / Arote="LTR39 repeat: matches 3 . 498 of consensus" 21609 . 21737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20003. .1030.
hotte-Aluss repeat: matches 1. .291 of consensus.
16482. .16641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 2. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is copies 2 mer ac 100% conserved"
19533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 copies 2 mer tg 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Alux reng
22878
                                                                                                                                                                                                                                                                         13523, .13820 /
/note="MLT1D re
13823, .13932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"AluJb
                                                                                           /note="LIMD 1
11947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"MIR
23452. 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Le-"LIMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          te-TIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18848. .18c
/note="13 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                             repeat_region
                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                           repeat_region
                                                                                                                                      repeat_region
                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
```

```
64428 CCTGGAGGAAATATCAGGGGGGGGGGGGTTAGGCGACTTGTCCCTAATTTTCGATGGGCC 64487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64488 ATACCTAATAGGCATAT-----TGAGCACAATGAAGGGAGAGAGATGATGAAGGTTT 64541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 64128 CACAGGCCATACTGGCTTCTCAGGTGGAAAAAATGAAATGTTAGAGTATAAAGTCAAGT 64187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64188 CCAGGGCTCTGAAITITAAAAGGTGCCTAGTAGGGCCTCTGTCCTCAGTGCTTAICAGTC 64247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        582 cgtatcettatgggggagetetetaateaccatgaccatcatgaatgtatgaetttgcettatg 641
                                                                                                                                                                                                                                                                                                                                                                                                123 gaggggetttaattggaggeeeegtagaggaegeegeggaacttetaaggtgggaaaa-- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 -----acgasattaasaatcetttgatatcagggetetgaateetgetggteagag 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462 atacccaataggcagatcaatgatgggatgggtggagatggagatgatatggaaatattc 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 caaccagaaaaaaaaaaateteateatggcaaatatteaceaggaaaacgaagagagg 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405 cctgcaggaaat---cgacggggacaggctcgccgacttgcccctaattttcgatgggcc 461
44 repeat: matches 5360. .5434 of consensus*
1600
                                /note-"LiM4 repeat: matches 2220. .2283 of consensus" 27601. .22975 peet: matches 3. .365 of consensus" 27976. .2873
                                                                                                                                                   Query Match 17.8%, Score 158.6; DB 9; Length 69648; Best Lond Similarity 60.1%; Pred. No. 1.3e-32; Indels 43; Gaps Matches 409; Conservative 0; Mismatches 229; Indels 43; Gaps
```

Page 13

Tue Mar 12 09:01:25 2002

```
repeat_region 2475. 2552. For the consequence of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 15.8%; Score 141; DB 9; Length 43952; Best Local Similarity 54.0%; Pred. No. 8,6e-28; Indels 76; Gaps Matches 494; Conservative 0; Mismatches 345; Indels 76; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36606 .36838 .
//note="Libhis repeat: matches 870. .640 of consensus"
36967 .37400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat: matches 490. .913 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat: matches 285. .419 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 428. .698 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 472. .576 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"MIR repeat: matches 101. 237 of consensus 35476. 35566 /note-"MIZD repeat: matches 1. 88 of consensus" 3564. 36167 /note-"MIZD repeat: matches 1. 88 of consensus" 3564. 36167 /note-"MIZD repeat: matches 1. 88 of consensus" 3643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sx repeat: matches 1. .136 of consensus;
repeat*
    19079. 19315
Anote-MRR repeat: matches 262. 13 of consensus
20482. 20770 repeat: matches 292. 9 of consensus
24479. 22522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat: matches 299. .1 of consensus"
IR repeat: matches 262. .13 of consensus"
20770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 43952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-
38934. 3902.
/note-"Limb6
3946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,3/99
/note="L1ME2
37979, 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note-Alu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT 13852 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
        epeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                        Numban.

Entrayota: Metazoa: Chordata; Craniata: Vertebrata: Euteleostomi; Eutrayota: Metazoa: Chordata; Craniata: Vertebrata: Euteleostomi; Mammania: Euthera: Primates; Catarrhini; Hominidae: Homo.

Entrayota: Burton.

Entred: Submission

Direct Submission

Losion 180, UK. E-mailenquires: Immquery@eanger.ac.uk Clone
requests: clonerequest@anger.ac.uk

INFORTANT: This sequence is the entire insert of clone U10564. The
true left and of clone U10564 is at 43952.

U10564 is from the Lawrence Livemore National Laboratory

flow-sortion/Oualifiers

Losetion/Oualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // Code mutching the match is the match in t
                                                                                                                                                                                                                              HSU105G4 43952 bp DAM 105G4, between markers DXS3G6 and DXS87 on Chromosome X contains ESTs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note-"LIMBB repeat: matches 520. ,920 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1121, 1233
/note-"LiMAl repeat: matches 61, 170 of consensus"
1121, 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .1203
.e="LIMB5 repeat: matches 61. .143 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat: matches 4965. .5390 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3155. 3463
Anote-Alusx repeat: matches 1. 300 of consensus
3465. 3568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5. .7612
te-"Alujo repeat: matches 302. .2 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 183. .261 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat: matches 118. .174 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3465, 358
//note=2.6 copies of 4 mer 88 % conserved*
4207, 4505
//note=*Alul repeat: matches 301, 1 of consensus*
4809, 56786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 1. .891 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 copies of 2 mer 100 % conserved. 17897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            copies of 2 mer 84 % conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /torganism="Homo sapiens"
/tb.xref="taxon:9506"
/cb.xref="taxon:9506"
/cbrowsome="x"
/clone_lib="LLOXNCO1"
/clone="LLOXNCO1-10564"
39. 420
            11622. .11659
/note=*19 cop1
                                                                                                                                                                                                                                                                                                                          292846
292846.1 GI:1877217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        te-"MIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .t. .7738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prim_transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                       RESULT 14
HSU105G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
```

FEATURES

COMMENT

දු පු

Oy 752 ttatttccatgt 763 Db 118 GAGATTGCATT 107

Search completed: March 11, 2002, 16:34:17 Job time: 8232 sec

```
X74118 B.bronchiseptica f
A73841 Sequence 1 from Pa
AF152500 Homo saptens pro
AK034641 Homo saptens cDN
AF217750 Homo saptens pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/organism="Mus musculus"
/bb_xrefe"=kaxon:10090
/chronosome="X"
/chronosome="X"
/inser_lex!"
/gene="Bex!"
/gene="Bex!"
/gene="Bex!"
/gene="Bex!"
/codou=tart=1

                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS AF097438 B35 bp mRNA ROD 11-APR-1999
LOCUS AF097438 B35 bp mRNA ROD 11-APR-1999
LOCUS COMPLET CAS.
ACCESSION AF097438.1 G1:4580589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 ATGGAGTCCAAAGATCAAGGCGTGAAAATCTCAACATGGAGAATGACCA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetGluSerLysAspGlnGlyValLysAsnLeuAsnMetGluAsnAspH1 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 luProAlaValAlaLeuIleSerGluAlaGlyLysAsnCysAlaProArg 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment_Scores:
Quality: 688.00 Length: 128
Ratio: 5.375 Gaps: 0
Percent Similarity: 100.000 Percent Identity; 100.000
      1315
1315
2382
2837
3547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AF097438 from: 1 to: 835
   22.97
22.97
44.54
52.61
65.08
   137.19
137.19
132.03
130.73
   93.50
93.00
93.00
93.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-327-750D-30 x AF097438
                                                                                                                                                  seq_name: gb_ro:AF097438
   gb_ba:BBFIMX
gb_pat:A73843
gb_pr:AF152500
gb_pr:AK024641
gb_pr:AF217750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
SOURCE
                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
MEDLINE
REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Len | Documentation | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 
                                                                                                                                                            About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
      OM of: US-09-327-750D-30 to: GenEmbl:* out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search information block:
Query: US-09-321-750D-30
Query length: 128
Databases: GenEmbl: *
Databases equences: 147214
Databases length: -343344837
Search time (sec): 4557.230000
                                                Date: Mar 11, 2002 3:33 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strd
+ +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence | 18t: Sequence | 18t
```

```
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: http://image.llnl.gov Series: IRAK Pitet: 9 Row: o Column: 6.
Location/Qualifiers
1. .2901
Corganism-Was musculus
(Ab_Aref="texton:10090"
Clone-Waciner: 7576 IMAGE: 15000522"
(Lissue-Lype-Wammary timnor. C3(1)-Tag model. Infiltrating ductal carcinoms. 5 month old virgin mouse."
(Ab_host-"MGICAR-MAGE: PCWV-SPORT6"
Colour-"MGICAR-MAGE."
(Ab_host-"PHIOR")
(Action of the Mage 
USA

VIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: Robert Strausberg, Ph.D.

Tel: (201) 465-1550

Email: Robert Strausberg*nih.gov

Email: Robert Strausberg*nih.gov

Dan Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIMI)

DNA Sequencing by: Baylor College of Medicine Human Genome

Center code: BWH-MSCS

Center code: BWH-MSCS

Contact: villaton*nwh age. Dem. tnc.edu/cdna/

Contact: villaton*nwh age. Dem. tnc.edu/cdna/

Contact: villaton*nwh age. Dem. tnc.edu, Hulyk, S., Lu, X., Garcia,

A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, M.,

Muzny, D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FHPSLGPLREELALAAGDALRPDASYARFLAARRGRAERVAALGRUPLARLGAUVAT
PHHHQUSHIRHLHUGODALHAASASYHPLIDPLASGSHLTRTPYPAGTLPPPLLDP
PLHBUSHURGRAEPROLPASLSAPKSAARQLAAHAGSASLGRAALBGOGOULAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 sGlnLysLysGluGluLysGluGluLysProGlnAspThrIleArgArgG 34 [Hill] [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GlyGlyArgArgArgArgPheArgValArgGlnProlleAlaHisTyrArgPr 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 118
Gaps: 0
Percent Identity: 99.153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPLHSVPLPAQEDYYSHLKKESDKPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: BC003254 from: 1 to: 2901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
Quality: 619.00
Ratio: 5:291
Percent Similarity: 99.153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-327-750D-30 x BC003254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                       REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
              /gene="Bex1"
/codon_statt=1
/codon_statt=1
/protein_id="AnADT168.1"
/protein_id="AnADT168.1"
/db_xree="Gi15702168."
/rranlation="HesRoDGVKNLNMENDHQKKEEKEEKPQDTIRREPAVALTSEAG
KNGAPRGGRREPRVQREPGHTRADDLANGRYGEPQGRRREBNYORFGGDVRGLMEKLER
S54 c 705 g 447 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia. Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dasea; Lo 7901)
Strausberg, R.
Direct Submission
Sibmitted (20-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MCC). Cancer Genomics Office. National Cancer Institutes, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS EC00324 2901 bp mRNA ROD 20-FEB-2001
LOCUS COCOSTAIN NUS MUSCALUS, Similar to dentatorubral pallidoluysian atrophy, ACCESION EC00324. mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 sGlnLysLysGluGluLysGluGluLysProGlnAspThrIleArgArgG 34 [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [111] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores;
Quality: 683.00 Length: 128
Quality: 5.378 Gaps: 0
Percent Similarity: 99.219 Percent Identity: 99.219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AF097437 from: 1 to: 2269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-327-750D-30 x AF097437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_ro:BC003254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGC.
house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
```

```
seq_documentation_block:
Locds HS198P4 35714 bp DNA PRI 16-DEC-2000
DEFINITION Human DNA sequence from clone RPI-198P4 on chromosome Xq22 Contains
ACCESSION ALCOB708 ALCOB708 ALCOB708 ALCOB708 HTG; CG Island.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exicano saplens
Exicaryofts; Metaroa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 35714)
Corby, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 CAACCAAGAAAATGAAGAAAAGGGG.......CAAGTEGCTAATAAAG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 ArgGluArgGlnLeuSerHisSerLeuArgAlaValSerThrAspProPr 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            455 AGGGAAAAGCAGTTGAGTCATAGTCTGCGGGCAGTCAGCACTGACCCCCC 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 pHisGlnLysLysGluGluLysGluGluLysProGlnAspThrIleArgA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetGluSerLysAsp. ..GlnGlyValLysAsnLeuAsnMetGluAsnAs 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 rgGluProAlaValAlaLeuIleSerGluAlaGlyLysAsnCysAlaPro 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 gTrpAspLeuMetGlnArgValGlyGluProGlnGlyArgMetArgGluG 83
                                                                                                                                                                                                                                                                                                                alignment_scores: Length: 129
Quality: 453.50 Gaps: 3
Percent Similarity: 89.147 Percent Identity: 68.992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .828
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tisuef_type="hypothalamus"
167. .544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AF220189 from: 1 to: 828
                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-327-750D-30 x AF220189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_pr:HS198P4
                                                                                                                                                                                                                                       256 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
     source
                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SW Homo sapiens
Evkaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi, Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi, Hammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

E (1 (bases 1 to 828)

A novel gene expressed in human hypothalamus

Unpublished

E (bases 1 to 828)

E (bases 1 to 828)
/translation-"MESKEKRAVNSLSMENANGENEEKEQVANKGEPLALPLDAGEYC
VPRGNRRRFWROPLIQYRMDMMHRLGEPQARMREENWERIGEEVRGLMEKLREKGLS
A 118 c 157 g 163 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS AF220189 818 bp mRNA PRI 04-MAY-2000
LOCUS AF220189 uncharacterized hypothalamus protein HBEX2 mRNA,
ACCESSION AF220189.1 G1:7689028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 gTrpAspLeuMetGlnArgValGlyGluProGlnGlyArgMetArgGluG 83
                                                                                                                                                                                                                                                                                                                                                                                                             16 pHisGlnLysLysGluGluLysGluGluLysProGlnAspThrlleArgA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 rgGluProAlaValAlaLeuIleSerGluAlaGlyLysAsnCysAlaPro 49
                                                                                                                                    alignment_scores:
Quality: 453.50 Length: 129
Ratio: 3.943 Percent Similarity: 69.147 Percent Identity: 68.992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 OHISHISASPHISHISASPGluPheCysLeuMetPro 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 TCACCATGACCATCATGATGAGTTTGCCTTATGCCC 377
                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AF183416 from: 1 to: 642
                                                                                                                                                                                                                                    alignment_block:
US-09-327-750D-30 x AF183416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_pr:AF220189
                                                           204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
```

```
/product="X-linked protein"
/product_ad="AAR3493.1"
/protein_id="AAR3493.1"
/translation="#ESKBERALNNLIVENVNQENDEKDEKEQVANKGEPLALPLANS
/translation="#ESKBERALNNLIVENVNQENDEKDEKEQVANKGEPLALPLANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homos splens
EUKATYOTS, Hetazoa; Chordata; Craniata; Vertebrata; Euteleostcoml;
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
10 (18889 12.0744)
10 (18889 12.0744)
11 (18889 12.0744)
12 (18889 12.0744)
13 (18889 12.0744)
14 (18889 12.0744)
15 (18889 12.0744)
15 (18889 12.0744)
16 (18889 12.0744)
17 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (18889 12.0744)
18 (1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dd dd coumnentation block: 744 bp mRNA PRI 15-APR-2001 DEFINITION Homo sapiens X-linked protein mRNA, complete cds. PRESION RESSION AF251053 GI:1362567
                                                                                                                                                                                                                                                                                                                                                                                                                      263 GGGAGCCC...TTGGCCCTCCCTTTGGATGCTGGAATACTGTGCCT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 ArgGluArgGlnLeuSerHisSerLeuArgAlaValSerThrAspProPr 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 gTrpAspLeuMetGlnArgValGlyGluProGlnGlyArgMetArgGluG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 rgGluProAlaValAlaLeuIleSerGluAlaGlyLysAsnCysAlaPro 49
                                                                       Ouality: 450.50 Length: 129
Secont Similarity: 88.372 Percent Identity: 68.993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualiflers
1. 744
7. Crganism="Homo sapiens"
/db_xref="taxon:9606"
101. 487
                                                                                                                                                                                                                                                             Align seg 1/1 to: AF237783 from: 1 to: 791
                                                                                                                                                                              alignment_block:
US-09-327-750D-30 x AF237783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_pr:AF251053
                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION A
VERSION A
VERYWORDS
SOURCE
DRIGHTHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens

Botaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 791); Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 791); May K., Xie,Y. and Mao,Y.M.

Novel Hungh, Y. Linked Brain Expressed Protein
Unpublished

Outpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ose_documentation_block:
191 bp mRNA PRI 02-SEP-2000
DEFINITION Homo sapiens brain-expressed protein BEX1 (BEX1) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="texon:9606"
/db_xref="texon:9606"
/chromosome="x"
1.799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Outdottage 1 to 791)
Mao,Y.M., Xie,Y., Yang,O.S., Wu,H., Lin,S. and Ying,K.
Direct Submission
Submitted (21-FEB-2000) Genetic Research Institute, Fudan
University, 220 Handan Rd., Shanghai 200433, P.R.China
Location/Oualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24120 AGAATATGGAAAGGATTGGGGAGGAGGTGAGACAGCTGATGGAAAAGCTG 24071
24308 CAACCAAGAAATGAAGAAAGGAG.......CAAGTTGCTAATAAAG 24268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 gTrpAspLeuMetGlnArgValGlyGluProGlnGlyArgMetArgGluG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 luAsnValGlnArgPheGlyGlyAspValArgGlnLeuMetGluLysLeu 99
                                                                                                       16 pHisGlnLysLysGluGluLysGluGluLysProGlnAspThrIleArgA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24020 TCACCATGACCATCATGATGAGTTTTGCCTTATGCCC 23984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 OHISHISASPHISHISASPGluPheCysLeuMetPro 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF237783
AF237783.1 GI:9963898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="BEX1"
172. .549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_pr:AF237783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
```

```
repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Alu repeat: matches 298. ,108 of consensus"
0593. ,10688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 11112. 11403
| //note-*Alu repeat: matches | 1. 308 of consensus*
| 11922. 12004
| //note-*L1 element fragment*
| 12062. 121308
| //note-*L1 element fragment*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ritial

yes-Mil repair matches 302. 1 of consensus*

110. .12916

Offs. .13081

110. .13532

113. .13532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tem. 11. vepeat: matches 1. .308 of consensus. 79. .22350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uete."29 copies of 2 mer 91 % conserved." 7496. 7874 of the fore."Lielement france."Lielement france."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /3. 15554
te="MLT2A1 element fragment"
71. 15928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73705. 23778
/note-*MLT1A element fragment*
23805. 23960
/note-*L1 element fragment*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Je24, .9731
/note="MLFIC element fragment"
3781, .9948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MLTIB element fragment"
23395. 23441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781. 9948
note-"MLTIC element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..... 1. element fragment" (49. .22995 te="Ll element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9890. .9948
/note="MLTIB element fragment"
10418. .10592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lA element fragment
                                                                                                                                                                                                                                                                                                                                  John Tragment 302. .8493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l element fragment"
19056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L1 element fragment" .23374
                                                                                                                                                                         note-"L1 element fragment"
2533, 4138
note-"match: multiple ESTS"
                                                                                                           /note-"Ll element fragment"
802. 988
/note-"Ll element fragment"
2533. 4138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71. 13940
te="L1 element fragment"
80. 18417
te="L1 element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   element fragment*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       element fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     element fragment"
                                                    /clone="GHC-870H8"
/clone_11b="SCCV"
475. 701
      /chromosome="X"
/map="X"
                                                                                                                                                                                                                                                                                                                               .8108
ote="L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8769. .9010
/note-"L1 ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95. .23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rtial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rtial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                           repeat_region
                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                      misc_feature
```

```
seq_documentation_block:

LOCUS
AL133148 40584 bp DNA PPI 06-MAR-2000
DEFINITION Human DNA sequence from clone RP1-79P11 on chromosome Xq21.32-22.1.
Contains the gene for a novel protein similar to mouse Bex2
(brain-expressed X-1nked protein 2), ESTs, STSs, GSSs and a putative Cp6 1sland, complete sequence.
ACCESION AL13334 6 GI:7076386
KEXMONEDS HTG; Bex2; CpG island.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sppiens
Bokaryota, Metacoa; Chordata; Cranista; Vertebrata; Euteleostomi;
Mammalia. Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (Dases I to 40584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (02-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 ISA, UK, E-mail enquiries: humquery@sanger.ac.uk Clone
24011 ...24541

/note-1.1 alement fragment*

2458. ...2470

/partal

/note-1.1 nopps

2429. ...10975

/note-1.1 alement fragment*

1.1 6129 g 9583 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 rgGlubrohlaValAlaLeuileSerGlualaGlyLysAsnCysAlaPro 49 (|||||| :::||||||| :::||||||| 3508 GGGGCCC...TrGGCCTACCTTAGARGTTAGARGATAGTGATAGTGTGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 pHisclnLysLysGluGluLysGluGluLysProGlnAspThrIleArgA 33
                                                                                                                                                                                                     alignment_scores:
Quality: 450.00
Guality: 3.979
Percent Similarity: 89.922 Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: HSV870H8 from: 1 to: 31321
                                                                                                                                                                                                                                                                                           alignment_block:
US-09-327-750D-30 x HSV870H8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_pr:AL133348
                                                                                                                           BASE COUNT 9462 a ORIGIN
                                                                                            repeat_region
                                        repeat_region
```

```
Homo sapiens
Makaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (pases 1 to 41029)
                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS HIGGORD 41029 bp DNA HTG 10-JUL-2001
LOCUS HIGGORD 40029 bp DNA BOOMEN SAUGURES CALLOXNCO1-8081 map q22.1-22.3, ***
ACCESSION ALOZIGE N PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venture tout: 3.

Venture tout: 1.

Venture tout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bitch C.
Submission
Submitted (109-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 18A, UK. Email enquiries: humquery6sanger.ac.uk
On Mar 12, 2010 this sequence version replaced gi:12750927.
Center: Sanger Center
Center: Code: SC
Center: Code: SC
Center: Code: SC
Center: Code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* the finished sequence as soon as it is available and

* the accession number will be preserved.

* LA 1029 cualifiers

/ Organism** Homo sepiens*

/ AD_ARCE** - tagon: 9606*
     alignment_scores:
Quality: 450.00 Length: 129
Ratio: 3.879 Gaps: 2
Percent Similarity: 89.922 Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment:00890"
PASE COUNT 13249 a 7796 c 7781 g 12203 t
ORIGIN
                                                                                                                         AL022169.3 GI:13276704
HTG; HTGS_PHASE2; HTGS_CANCELLED.
human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="x"
/map="521.1-22.3"
/map="11.22.3"
/clone="11.0xNc01"
/clone="11.0xNc01"
1. 41029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-327-750D-30 x HSU80Bl
                                                                                                                                                                                                                                                                                             seq_name: gb_htg:HSU80Bl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
Em: A199470 Em: AA319216 Em: AA317625 Em: D81392 Em: AA317418
Em: AA366528 Em: C15186 Em: A129270 Em: AA612605
Em: AA366528 Em: C15186 Em: A129272 Em: EA4612605
Em: AA16082 Em: A1284405 Em: A4160657 Em: AA612605
Em: A416172 Em: A436405 Em: A4161705 Em: A4161106
Em: A4161705 Em: A414172 Em: A4464652 Em: A4162706
Em: A68380 Em: A4164162 Em: A4364655 Em: A446471 Em: A4865227
Em: A68380 Em: A4164162 Em: A4164705 Em: A446477 Em: A4866327
Em: A483998 Em: A156466 Em: A4167701 Em: A1629428
Em: A44379411 Em: C15948 Em: AA714565 Em: A4167929428
Em: A4779411 Em: C15948 Em: AA714565 Em: A4179791
/evideme-enc. expecimenta.
/evideme-enc. expecimenta.
/evideme-enc. expecimenta.
/coopt-enent(170811.1)
/gene-enf/79911.1]
/gene-enf/79911.1]
/gene-enf/79911.1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30411. 30922.

30411. 30922.

Anote-'note 1stand match: STS: Em:H61107*

31431. 31262.

Anote-'note 1stand match: STS: Em:A61107*

3147. 31130.

Anote-'note 2 mer cc 64% conserved*

Complement(3265. 31316).

Anote-'note 34144.

Anote-'note 34146.

Anote-'note 34186.

Anote 34186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30507. .3098a.11.
30508. .3062.
30508. .3062.
30508. .3062.
30508. .3062.
30508. .3052.
30541. .30523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11032 GGGAGCCC...TTGGCCCTTGAATGTTAGTGAATACTGTGTGCCT 30986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 ArgGluArgGlnLeuSerHisSerLeuArgAlaValSerThrAspProPr 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 gTrpAspLeuMetGlnArgValGlyGluProGlnGlyArgMetArgGluG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 luasnValGlnargPheGlyGlyaspValargGlnLeuMetGluLysLeu 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 rgGluProAlaValAlaLeuIleSerGluAlaGlyLysAsnCysAlaPro 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: AL133348 from: 1 to: 40584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
Quality: 450.00 Length: 129
Ratio: 3.879 Gaps: 2
Percent Similarity: 89.922 Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-327-750D-30 x AL133348/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
```

```
| ALS82060 ALS82060 LT_NFL
| BIO40889 QV3-NF0278-1202001
| AM93488 RC1-DF0001-230200
| AM934405 RC1-DF0001-230200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REMUMBLIS; EUCHETIA; ROUGHILDS; SCIIIUSHIALIN; MILLIAGE, MILLIAGE, REMUMBLIS; EUCHETIA; ROUGHILDS; SCIIIUSHIALIN; MILLIAGE, MILLIAGE, A., Chandra, I., Mason, T.M., Quackenbush, J., Ratlage, A.R. and Adams, M.D.
RATLAGGE, A.R. and Adams, M.D.
Gene Index Project: Generation of a Rat EST (REST) Catalog & Rat Generation of a Rat EST (REST) Catalog & Rat Generation of a Rat EST (REST) Catalog & Rat Generation of a Rat EST (REST) Catalog & Rat Generation of a Rat EST (REST) Catalog & Rat EST (REST)
                                                                                                                                                                                                                                                                  ACCESSION A1227867.1 GI:3811754
VERSION A1227867.1 GI:3811754
VERSION A1227867.1 GI:3811754
VERSION A1227867.1 GI:3811754
VERSION Rattus sp.
ORGANISM Rattus sp.
ORGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: AI227867 from: 1 to: 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:

Quality: 620.00
Gaps: 0
Percent Similarity: 99.153
Percent Identity: 99.153
    594.05 6.3e-24
593.18 7.1e-24
589.55 1.1e-23
589.38 1.2e-23
588.78 1.2e-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-327-750D-34 x Al227867/rev
    356.50
+ 355.00
+ 355.00
+ 355.00
                                                                                                                                                                                                                seq_name: gb_est1:AI227867
         gb_estl:AL582060
gb_est2:BIO40889
gb_estl:AW934883
gb_estl:AW934905
gb_estl:AW934769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Command line parameters:
-WODEL-frame-p2n.model -DBV-xlh
-WODEL-frame-p2n.model -WARN-p1n.model -DBC-p2n.model
-WODEL-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2n.model-frame-p2
                                                                                                                                                 About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM of: US-09-327-750D-34 to: EST:* out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ## Orlg

## Strd

## 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search information block:
Ouery US:09-127-750D-34
Ouery Length: 118
Database: EST:** EST:** Established Batabase Instyle 11351937
Batabase Instyle: 107921985
Search time (Sec): 4085.940000
                                                                             Date: Mar 11, 2002 2:16 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Seq
```

```
/orgalia="Mus musculus"
/orgalia="Mus musculus"
/db_xref="blsiple_dr"
/db_xref="blsiple_dr"
/db_xref="blsiple_dr"
/db_xref="blsiple_dr"
/db_xref="blsiple_dr"
/db_xref="blsiple_dr"
/clone="24/1004Mis"
/clone="tallodwis"
/clone="tallodwis"
/clone="tallodwis"
/colon_stative
/col
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDRN was primed with a primer file Schackandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandschockandsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 AIGGCATCCAAATTTAAACAAGTCATACTGGATCTCACTGTGGAGAAGA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 lnValMetGluAlaLysArgHisSerLysGluGlnGlnMetArgProTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ThrargPheargThrProGluproAspasnH1sTyrAspPheCysLeuIl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 erHisHisLeuGluGluValGluAsnLysLysProGlyGlyAsnValArg 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetalaSerLysValLysGlnValIleLeuAspLeuThrValGluLysAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AK010400 from: 1 to: 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="putative"
161 c 205 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //0. .775
/note="putative"
789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-327-750D-34 x AK010400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1107668 1 to 789)

5 The RIKEN Genome Exploration Research Group Phase II Team and the FANTON Consortune of a full-length mouse cDNA collection
FANTON CONSORTUNE (1978)

NEUTRICONSTANT (1978)

Adachla. Alzawa. K. Akahlas. S. Akimura. T. Aono, H. Aral. A. Arawa. F. Cannoci. P. Futuda. S. Akimura. T. Arawa. T. Carnoci. P. Futuda. S. Akimura. T. Arawa. T. Grono. H. Xendi. M. Haracka. T. Futuda. M. Haracka. T. Futuda. M. Haracka. T. Hori. T. Horo. H. Koyla. N. Kurlhara. C. Matsyman. T. Minozaki. A. Konno. H. Xouda. M. Haracka. M. Karaki. T. Kollan. Y. Sound. H. Xouda. M. Yanmazali. R. Mahli. T. Nono. H. Xouda. M. Yanmazali. R. Mahli. T. Suruk. H. Togama. M. Yanmazali. R. Sandi. T. Suruk. M. Yangama. T. Sandi. C. Salto. H. Saklo. R. Saklo. M. Saklo. H. Sandi. T. Togian. Y. Togan. T. Yangama. Y. Sannishi. P. Togalia. Y. Yangan. M. Tagama. M. Tagama. M. Tagama. T. Saunishi. P. Togalia. Y. Suruk. H. Yangama. Yangawa. Takahashi. P. Direct Submission on M. Muramatsu. M. and Hayashizaki. The Institute of Physical and Chemical Research (FARN). Jaboractor for Genome Exploration Research Group. Rike Genome Szpioration Research Group. Par. 81 - 45-503-9222. Par. 81 - 45-503-9222. Par. 81 - 45-503-9222. Par. 81 - 45-503-9222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (base 1 to 789) Shibata, Y., Hayatau, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okezati, Y., Muramatau, M. and Hayashizati, Y. Normalization and aubtraction of age rapper selected cDNAs to Genome research. 10 (10), 1817-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.08ces 1 to 789)
Shibata, K. Itoh, M. Alzava, K. Nagaoka, S., Sasaki, N., Carninci, P., Shibata, K. Itoh, M., Alzava, K., Kitsunai, T., Tashito, H., Itoh, M., Sumi, N., W. Ishii, Y., Wakamure, S., Hazama, M., Wishine, T., Harda, A., Forjavak, T., Kashine, T., Harda, A., Forjavake, S., Inoue, M., Sakaguchi, S., Itoegami, T., Kashiwagi, K., Forjavake, S., Inoue, K., Togava, Y., Tara, M., Chara, E., Warthiki, M., Okazaki, Y., Muramatsu, M., Tonoe, Y., Tanaka, T., Matsura, S., Kavai, J., Okazaki, Y., Muramatsu, M., Tonoe, Y., Kita, A. and Hayashizaki, Y. sequencing plenia settle sequence analysis (RISA) system-384-format Genome sesarch, 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          further details.

Model interpretation of the property of the property of the property of the property of denome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotts, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Entheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 78) Rodentia; Sciurognathi; Muridae; Mus. Carnincis P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Methods in enzymology. 303, 19-44 (1999)
                                                                                                                                                                       AKO10400

AKO10400

AKO10400

AKO10400

AKO10400

AKO10400

AKO10400.1 G1:12845816

AKO1040.1 G1:12845816

AKO1040.1 G1:12845816

AKO1040.1 G1:12845816

AKO104.1 G1:12845816

A
                                                                         seq_name: gb_htc:AK010400
                                                                                                                                                                                      seq_documentation_block:
LOCUS AK010400
DEFINITION Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
```

TITLE

COMMENT

TITLE

```
Licottion/Qualifiers

1. 540

Astain="Sprague-Dawley"

/drain="Sprague-Dawley"

/drain="Sprague-Dawley"

/drain="Sprague-Dawley"

/drain="Sprague-Dawley"

/drain="Sprague-Dawley"

/drain="Ur-R-BDO-dah-D-06-0-Ur-

/clone="Ur-R-BDO-dah-D-06-0-Ur-

/drain="Ur-B-Dawley"

/drain="Ur-B-B-Dawley"

/drain="Ur-B-B-Dawley"

/drain="Ur-B-B-Dawley"

/drain="Ur-B-B-Dawley"

/drain="Ur-B-B-Dawley"

/drain="Ur-B-B-Dawley"

/drain="Ur-B-B-B-Dawley"

/drain="Ur-B-B-Dawley"

/drain="Ur-B-B-B-Dawley"

/drain="Ur-B-B-B-B-Dawley"

/drain="Ur-B-B-B-B-Dawley"

/drain="Ur-B-B-B-Dawley"

/drain="Ur-B-B-B-B-B-B-B-B-B-B-B-B-B-B-B-B-B-B
                                                                                                                                                                                                                                          Contact: Soares, MB
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of East Gene Discovery and Mapping
University of East Gene
University of East State State
151 313 518 519
Pat: 319 315 518 519
Pat: 319 315 518
Pat: 319 518
Pat: 319 518
Pat: 318
Pat: 319 518
Pat: 318
Pat: 319 518
Pat: 318
Pat: 3
1 (bases 1 to 540)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Gallicovery
Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 rgleuvalproksnPheLeuTrpalalleProksnArgHisValAspHis 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 LysGlyClyLysAlaSerLysGlnSerGluGluGluSerHisHisLeuGl 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: AW251884 from: 1 to: 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                520.00 Length: 97
5.417 Gaps: 0
98.969 Percent Identity: 98.969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAG_SEQ=GATTC*
TAG_SEQ=GATTC*
120 c 94 9 180 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-327-750D-34 x AW251884/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                   JOURNAL
MEDLINE
COMMENT
                                                                              REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
    Norway rat.
Narus norvegicus
Enkarus norvegicus (Chordata, Craniata; Vertebrata, Buteleostomi)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AF21884 540 bp nRNA EST 17-DEC-1999
DEFINITION U1-R-BJO-adn-b-06-0-U1.sl U1-R-BJO Rattus norvegicus cDNA clone
U1-R-BJO-adn-b-06-0-U1.sl U1-R-BJO Rattus norvegicus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 sAsnLysLysGlyGlyLysAlaSerLysGlnSerGluGluGluGluSerHisH 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 etGluAlaLysArgHisSerLysGluGlnGlnMetArgProTyrThrArg 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AA473525 from: 1 to: 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW251884
AW251884.1 GI:6595475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-327-750D-34 x AA473525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est1:AW251884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                          FEATURES
SOUTCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
```

```
155
                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                      MdI:1471479

MdI:1471479

Seq primer: 40RP from Gibco

Seq primer: 40RP from Gibco

High quality sequence stop: 472.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Ado,xref-taxon:10090*

Ado,srage*mmnsupulus*

Ado,srage*mmbryo, 10:5 dpc*

Ado,srage*mbryo, 10:
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS BE31374 463 bp mRNA EST 14-JUL-2000
DEFINITION U927h06;13 Soares_NMEBA_Dranchial_arch Mus musculus CDNA clone
DEFINITION 1927h06;13 Soares_NMEBA_Dranchial_arch Mus musculus CBNA clone
IMAGE:1368347 5' similar to SW:HG74_HUMAN Q00994 OVARIAN GRANULOSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 erHishisLeuGluGluValGluAsnLysLysProGlyGlyAsnValArg 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 lnValMetGluAlaLysArgHisSerLysGluGlnGlnMetArgProTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: BF723075 from: 1 to: 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-327-750D-34 x BF723075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est1:BE333774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                           FEATURES
```

```
ACCESSON RE13174.0 KD PROTEIN SGR14.;, mBAN sequence, VERSION RE13174.1 GI:9207550

KEYWORDS

SETT TO THE PARTY OF THE PAR
```

```
wis misschies

BURATYOTE, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Manmalla; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Mus.
(Bases Ito 472)

RATTAR, Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kuchba, T., Lacy, M., De, M., Marthn, T., Morris, M.,
Theksing, B., Wylte, T., Lennon, G., Soares, B., Wilson, R. and
Macerson, R. asab, Hus, T., Lennon, G., Soares, B., Wilson, R. and
The Sab, Theksing, B., Wylte, T., Lennon, G., Soares, B., Wilson, R. and
The Sab, Theksing, B., Wylte, T., Lennon, G., Soares, B., Wilson, R. and
The Mass Mouse EST Project
                                                                                                                                                                                                                                                          1...444.
/Octanian="Ratius sp."
/Octanian="Ratius sp."
/Clone="RELAYS"
/Clone=lib="Normalized rat placenta, Bento Soares"
/note="Octan: placenta; Vector: pT773Pac; Site_1: EcoRi;
site_2: Not!" 81 g . 124 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            documentation block:

472 bp mRNA EST 14-MAY-1986
DEFINITION m55909.rl Goares mouse embryo NDME13.5 14.5 Mus musculus cDNA Clone MAGE:357288 5 smallbr to SN:4074_HUMAN 00094 CVMARAN GRANULOSA CELL 13.0 KD PROPER MERA'- [1] ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marta MyMouse EST Project
Mashlo-HHWI Mouse EST Project
Mashington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
9712, Medical Center Drive, Rockville, MD 20850, USA El: (301) 838-532 Fax: (301)-838-5038 Fax: (301)-838-0308 Email: nheeftlyr.org Seq primer: M13-21. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: AI012535 from: 1 to: 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores: Length: 80 | Length: 80 | Ratio: 5.462 | Gaps: 0 | Percent Similarity: 97.500 | Percent Identity: 97.500 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-327-750D-34 x AI012535/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W35893.1 GI:1317733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est2:W35893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                        FEATURES
/clone-'IMAGE:538606'
/clone-'IMAGE:538606'
/clone.lhe-Beddington mouse embryonic region'
/stx-Pooled'
/tissue_type-'embryo'
/de_tstage-'7.5dpc'
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus sp.
Rikaryosp.
Bikaryosp. Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalla; Euthería; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 444).

(base M., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Karlavage, A. and Adams, M.D.

Rar Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS A012335 444 bp mRNA EST 15-JUN-1998
LOCUS SET 15-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 lnValMetGluAlaLysArgHisSerLysGluGlnGlnMetArgProTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 erHisHisLeuGluGluValGluAsnLysLysProGlyGlyAsnValArg 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene Index
(Onpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AA117429 from: 1 to: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-327-750D-34 x AA117429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est1:AI012535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
```

Page 11

1 MetAlaSerLysValLysGlnVallleLeuAspLeuThrValGluLysAs 17

Align seg 1/1 to: AL118340 from: 1 to: 422

alignment_block: US-09-327-750D-34 x AL118340

Percent Identity: 87.288

Tue Mar 12 09:01:44 2002

```
240 CAAAAAAGACAAAAAGGTGGGAAGGCCTCCAAACAAAGTGAAGAAGAAC 289
                                                                                                                                                                                                                                                                                      17 pLysLysAsnLysGlyGlyLysAlaSerlysGlnSerGluGluGluS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 gHisValAspHisSerGluGlyGlyGluGluValGlyArgPheValGlyG 84
                                                                                                                                Align seg 1/1 to: BG083261 from: 1 to: 792
                                              alignment_block:
US-09-327-750D-34 x BG083261
Percent Similarity: 93.220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 ePro 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             540 ACCT 543
                                                                                                                                                                                                                                                                                                                                                                                   house mouse.

Sharm manuals.

Sharm manuals.

Sharm manuals.

Sharm manuals.

Mammalia: Eucheria; Rodentia; Craniata; Vertebrata; Euteleostomi;

Mammalia: Eucheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Skargul, CJ,, Dudekula, D.B., Qlan, Y., Lim, M.K., Jaradat, S.A., Tanaka

"T.S., Carter, M.G. and RO, M.S.H.

"T.S., Carter, M.G. and RO, M.S.H.

"T.S., Carter, M.G. and RO, M.S.H.

"T.S., Carter, M.G. and Appropriation of NIA mouse 15K *CDNA clone set

"T.S., Carter, M.G. Sharm and Appropriation of NIA mouse 15K *CDNA clone set

"T.S., Carter, M.G. Suite 4000. Baltimore, MD 2124-6820, USA

"This clone set has been freely distributed to the community. Please

"This clone set has been freely distributed to the community. Please

"This clone set has been freely distributed to the community. Please

"This clone set has been freely distributed to the community. Please

"This clone set has contain in an in gov, CDNA/15k, html for details.

"Thy quality sequence stop: 792

POURANCE OLIMANOLICE STOP: 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              libraries.
/lab.nost-DHIOB.
/lab.nost-DHIOB.
/lock-Wector; pSPORTI; Site_1: Sali; Site_2: NOII; This clone a mong a rearrayed set of 15,447 clones from 11 clone is among a rearrayed set of 15,447 clones from 11 clone is among a rearrayed set of 15,447 clones from 11 part of 27.5 embryos.

part of ET; embryos: extrementyonic part of ET; embryos and EL2.5 fembryos is and EL2.5 fembryos overy cONA ilharry average insert size 1; kb. All source libraries are cloned unidirectionally with Oilgo(df ).Not primers. References include: (1) Genome wide expression profiling of mid-gestation placents and embryoushing a 15,000 mouse developmental cDNA microarray, 2000, Large-scale CDNA analysis reveals phased gene expression perterns during preinfolantiation mouse development, 120: 1337-1745; (3) Genome-wide mapping of 7.5-494 mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Gener 7: 1967-1978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. 792
Acran. Was musculus"
Acran. CS7BL/61*
Acran. CS7BL/61*
Clone. 11b- With Mouse 15K CDNA Clone Set"
Asx-Clones arrayed from a variety of CDNA libraries"
Acran. Clones arrayed from a variety of CDNA
                                                                                                                                                                                                           seq_documentation_block: 792 bp mRNA EST 26-JAN-2001 LOCOS BG008261 792 bp mRNA Clone Set Mus musculus cDNA clone ACCESSION H3086C08 5', mRNA sequence. ACCESSION BG083261.1 GI:12555829
508 AGGCGTTTCCGAACCCCGGAACCTGACAATCATTACGACTTTTGCCTCAT 557
                                                                                                                                                             seq_name: gb_est2:BG083261
                                                     117 ePro 118
                                                                                                           558 ACCT 561
                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
```

Muse mouse.

Mus musculus

BLARIYOTA, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;

Mannalis, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Marrah, Hiller, Allen M. Bowless M., Dietrich, N. Dubuque, T.,

Gelsel, S., Willer, T., Lacy, M., Le. M., Martin, J., Morris, M.

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and

Materston, R. Email: mouseestévatson.vustl.edu This clone is available royalty-free through LLML; contact the TMGE Consoctium (infoéimage.lln1.gov) for further information. MG:51138 AA473255 1458 bp mRNA EST (18-JUN-1997)
vg/9809.11 Barsteed WDFRRAL WHO BENECHLUS. CDNA CLORE INTRETENTAGES
similar to SWHHG74 HUMAN Q00994 OVARIAN GRAWULOSA CELL 13.0 KD
PROTEIN HGR74.; mRNA sequence. Matta-Jour, M.
The MashD-HBMI Mouse EST Project
Unpublished (1995)
Contact: Marza M/Mouse EST Project
MashI-HBMI Mouse EST Project
M Seq primer: -28ml3 rev2 ET from Amersham 11gh quality sequence stop: 417. AA473525 AA473525.1 GI:2201752 seq_name: gb_estl:AA473525 seg_documentation_block: LOCUS AA473525-DEFINITION vg78a09.rl Ba ACCESION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT

alignment_scores: Quality: 546.00 Ratio: 4.964

TUE

247

BASE COUNT

Page

```
Location/Qualifiers

Location/Qualifiers

1. :540

/organiam-Rattus norvegicus*
/drain-Sprague-Dawley*
/db.grain-Sprague-Dawley*
/db.grain-Sprague-Dawley*
/db.grain-Sprague-Dawley*
/dc.grain-Wir-BJU
/dc.grain-W
                                                                                                                                                                                                    Contact: Soares, MB
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Independent Research Building lowa City, IA 52242, USA
451 Eckstein Medical Research Building lowa City, IA 52242, USA
781: 319 315 855
Raxi: maoares@blue.weeg.ulowa.edu
The soarence contained an oiigo-df track that was present in the
Oilgonoulcectde that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail: The sequence tag present in the CDNA between the Noil site
and the oilgo-df track served to identify it as a clone from the
normalized actium at 16.5 do ilbrazy Preparation:
M.B. Soares tabb Clone distribution: clones will be available
Seg prime: M3 Formard
POLYA-Yes
                                                          T. (bases 1 to 540)
T. (bases 1, Lennon, G. and Soares, M.B.
Soanaldo, M.F., Lennon, G. and Soares, M.B.
Soanalide, M.F. (action of the paper of the contract of the pene
       Mammalla; Butherla; Rodentla; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rgLeuValproAsnPheleuTrpalalleProAsnArgHisValAspHis 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: AW251884 from: 1 to: 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAC_LIB-UI-R-BJO
TAC_TISSUE-atrium at 16.5 dpc
TAC_SEQ-GATTC*
120 c 94 q 180 t
                                                                                                                               discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-327-750D-34 x AW251884/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                             REFERENCE
AUTHORS
TITLE
                                                                                                                                                                JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
Norway rat.
Rattus norvegicus
Bukaryos: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCOS ANATS1884 540 bp mRNA EST 17-DEC-1999
LOCOS ANATS1884 540 bp mRNA EST 17-DEC-1999
ANATS1884 The BJO-40-0-06-0-01.sl UT-R-BJO Rattus norvegicus CDNA clone
ACCESSION ANATS1884 1 G1:6595475
VERSION ANATS1884 1 G1:6595475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 AGACAAAAAGGTGGGAAGGCCTCCAAACAAAGTGAAGAAGAAGAACCCCACC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 etGlualaLysArgHisSerLysGluGlnGlnMetArgProTyrThrArg 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 sAsnLysLysGlyGlyLysAlaSerLysGlnSerGluGluGluSerHisH 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 PheArgThrProGluProAspAsnHisTyrAspPheCysLeullePro 118
313 TrocGAACCCGGAACCTGAAARCARTACGACTTGCCTCARACCTGACARTACGACTTACCCTARACCTGACARTACGCTGAACCTGACAGCTGAAARCARTACGACTTACGCTGAACCCTGAAARCARTACGACTTACGCTGAACCCTGAACCCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AA473525 from: 1 to: 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-327-750D-34 x AA473525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_est1:AW251884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
              FEATURES
```

Tue Mar 12 09:01:21 2002

hommy

```
/organism-"Homo sapiens"
/organism-"Homo sapiens"
/organism-"Homo sapiens"
/clone_ilb-"Noil_CGAP_Lyml2*
/clsue_type-"lymphoma, follicular mixed small and large
cell"-"Lype-"lymphoma, follicular mixed small and large
/lab_host="DHIOB"
/lab_host="PHIOB"
/lab_host="P
169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
```

alignment_scores:

| Quality: 609.00 | Length: 111 | Ratio: 5.466 | Gaps: 0 | Percent Similarity: 100.000 | Percent Identity: 100.000

alignment_block: US-09-327-750D-13 x AW512400/rev

Align seg 1/1 to reverse of: AW512400 from: 1 to: 612

- 1 MetalaAsnIleHisGlnGluAsnGluGluMetGluGlnProMetGlnAs 17

seq_name: gb_estl:AI193112

LOGUS A1193112 615 bp mRNA EST (29-OCT-1998)
DEFINITION QE66909.x1 Scarces fetal, Lung, MbHL19W Homo Sapiens FORM CIONE
IMAGE:174428 3' similar to gb.#38188 OYARIAN GRANULOSA CELL 13.0
KD PROTEIN HGR74 (HUMAN);, mRNA sequence. seq_documentation_block: LOCUS A1193112

A1193112 A1193112.1 GI:3744321

human. Homo sapiens ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Mominidae; Momo.

E. 1 (bases I to 615)

NGI-GOAP http://www.nobi.nim.nih.gov/noiogap.

National Cancer Institute. Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Tumor Gene Index

Conteact: Robert Strausberg, Ph.D.

Email: Gappbar remail.nih.gov

This clone is availlable royalty free through LLNL; contact the INAS Conscitutum (info@mange.llni.gov) for further information.

Index Conscitutum (info@mange.llni.gov) for further information.

Seg primer: -400P from Gibso.

Localion/Qualifiers

Localion/Qualifiers

Tocalion/Qualifiers FEATURES Source BASE COUNT ORIGIN JOURNAL REFERENCE AUTHORS TITLE

169 a

alignment_block: US-09-327-750D-13 x AI193112/rev

Align seg 1/1 to reverse of: Ali93112 from: 1 to: 615

67 tGlullePheMetGluGluMetArgGlulleArgArgLysLeuArgGluL 84

84 euGlnLeuArgAsnCysLeuArgIleLeuMetGlyGluLeuSerAsnH18 100

101 HisaspHisHisAspGluPheCysLeuMetPro 111

us-09-327-750d-(13)rst

```
Homes septems
Enkarycra Hetazoa, Chordata; Cranlata; Vertebrata; Euteleostomi;
Enkarycra; Hetazoa, Chordata; Cranlata; Vertebrata; Euteleostomi;
Hammalia; Eutheria; Primates; Catarrinin; Hominidae; Homo.

1 (base 1 to 662)
Hiller, L., Allan, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Len, N., Lennon, G., Marra M., Martin,
J., Woore, B., Schellenberg, K., Steptoce, M., Ra, F., Thetsing, B.,
Miller, Y., Wyller, Naterston, R. and Wilson, R., Thetsing, B.,
Mashington University School of Medicine
Mashington University School
Mashington Mashington Mashington
Mashington Mashington
Mashington Mashington
Mashington Mashington
Mashington Mashington
Mashington Mashington
Mashington
Mashington
Mashington
Mashington
Mashington
Mashington
Mashington

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/organism="Homo sapiens"
/ob_xref="Exacon:900"
/clone_lib="Schneider fetal brain 00004"
/clone_lib="Schneider fetal brain 00004"
/sex="male"
/sex="male"
/sex="male"
/sex="male"
/sex="male"
/sex="male"
/de jagge="foncing post-conception"
/de jagge="foncing post-conception"
/de jagge="foncing post-conception"
/de jagge="foncing post-conception"
/note="organ: brain; vector; pBluescript äk (Stratagene);
/note="organ: brain; vector; pBluescript äk (Stratag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence:
5'-GagadagagaagaggtCaaggaTCCTTAATTAAATTAATCCCCCCCCCCCCC-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_estl:AI929106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1...620.
1..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ph.D.

CONA Library Preparation: M. Bento Soares, Ph.D.

CONA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Rashington University Genome Sequencing Center

Clone distribution: NRI-CGAP clone distribution information can be
found through the I. M.A.G. E. Consortium/LiNL at:

How-tho.llnl.gov/bbrp/image/lmage.html

Insert Length: 725 std Error: 0.00

Seq primer: 40013 fwd. Er from Amersham

High quality sequence stop: 339.

Location/Qualifiers:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Bukarryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Bukarryota, Metazoa, Chordata, Catarrhini, Hominidae; Homo.
1 (bases 1 to 620)
1 (bases 1 to 620)
1 (cota http://www.ncbi.nlm.nih.gov/ncitcgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Outeact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Ggapbar rémail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
                                                                                                                                                                                                                                                                                                                    LOCUS A557696 620 bp mRNA EST 12-SEP-1997
DEFINITION NMBAD404.81 NOT.CAPP.CO9 Homo septens CDNA close IMAGE:1074727 3'
SIMILAT LOG9:H8188 OVNRIAN GRANILOSA CELL 13.0 KD PROTEIN HGR74
ACCESSION A5776958 I GI:2354432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: AA576958 from: 1 to: 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 c 116 g 191 t
284 CATGACCATCATGATGAATTTTGCCTTATGCCT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-327-750D-13 x AA576958/rev
                                                                                                                                                                           seq_name: gb_estl:AA576958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
```

and 3' adaptor sequence.

3'. CakakakakakcrCakarrrrrrrrrrrrrrrrrr. ''. The library wa size-selected for >0.5 kb inserts and has an average insert size selfamated at 1.7 kb. This library was constructed using the CAP-trapper method for full-length

```
11 (mouse)
```

/note="putative" 208 a 211 c 227 g 790. .795 /note-"putative 809 polyA_signal polyA_site BASE COUNT ORIGIN

alignment_scores:
Quality: 688.00 Length: 124
Ratio: 5.548 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.387

alignment_block: US-09-327-750D-12 x AK004531

Align seg 1/1 to: AK004531 from: 1 to: 809

1 MetalaasnValHisGlnGluAsnGluGluMetGluGlnProLeuGlnAs 17

34 lyAsnAsnAsnAsnAsnAsnAsnHisAsnHisAsnHisAsnHisHisArgArg 50

84 etGluGluWetArgGluIleArgArgLysLeuArgGluLeuGlnLeuArg 100 101 AsnCysLeuArglleLeuMetGlyGluLeuSerAsnHisHisAspHisHi 117

seq_name: gb_est1:AA253897

my31e10 r1 Barstead mouse pooled organs WELRMA HUS THR-1927 clone IMAGE:697482 5' similar to gb:H38188 0VARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74 (HUMAN);, mRNA sequence. AA253897.1 GI:1888253 seq_documentation_block: Locus AA253897 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

house mouse.

Mus musculus

Bukaryora, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryora, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 460

Mannalia; Euteria, Rodoniia; Sciurognathi; Muridae, Mus.

1 (bases 1 to 460

Maria, M., Millaria, Bowles, M., Dewi, Martin, J., Mortis, M.,

Geisel, S., Kuchar, T., iacy, M., Lew, Martin, J., Mortis, M.,

Theising, B., Kieptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and

Materston, R. and Mylouse EST Project

Contact: Marra M/Mouse EST Project REFERENCE AUTHORS

TITLE JOURNAL COMMENT

HashD'HHMI Mouse EST Project
HashIngton University School of MedicineP
HashIngton University School of MedicineP
144 Forest Park Park Park Way
141 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810 And of the control of FEATURES

BASE COUNT ORIGIN

alignment_scores:

Quality: 687.00 Length: 124
Ratio: 5.540 Gaps: 0
Percent Similar!!v: 100.000 Percent Identity: 97.581

alignment_block: US-09-327-750D-12 x AA253897

Align seg 1/1 to: AA253897 from: 1 to: 468

34 lyAshAshAshAshAshAshHisAshHisAshHisAshAshAshGarg 50

84 etGluGluMetArgGluIleArgArgLysLeuArgGluLeuGlnLeuhrg 100

101 AsnCysLeuArgIleLeuMetGlyGluLeuSerAsnHisHisBHisHi 117

117 sAspGluPheCysLeuMetPro 124

/db_xref="taxon:1090"
/db_xref="taxon:1090"
/clone_ilb=Barstead mouse pooled organs MPLRB4*
/clone_ilb=Barstead mouse pooled organs MPLRB4*
/sxe="alkad"
/tissue_type="pooled organs"
/de_tstage="7 day"
/d

168

11(mosae)

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryotan Mataoa; Chordata, Craniata; Vertebrata, Buteleostomi; Bukaryotan Metaoa; Chordata, Sciurognathi; Muridae; Murinae; Musinamalia; Eutherita; Rodentia; Sciurognathi; Muridae; Murinae; Musinamalia; Eutherita; Rodentia; Sciurognathi; Muridae; Musinae; Lo 612)

Ratza, M. Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubque, T., Gelsel, S., Kucaba, T., Lacy, M., Lem, F., Undartond, K., Moorse, B., Materston, R., Steptoe, M., Tan, F., Undarwood, K., Moorse, B., Materston, R., Steptoe, M., Tan, F., Undarwood, K., Moorse, B., Materston, R., Steptoe, M., Tan, F., Undarwood, K., Moorse, B., Materston, R., Eproject

Unpublished (1998)

The Name of the Steptoe of Medicine Mashington University School of Medicine Mashington University School of Medicine Mashington University School of Medicine Passilla 286 1800

Fax: 314 286 1800

Email: mouseestfwatson, wustl. edu

Fills clone is available royally-free through LLML; contact the IMAGE Consortum (infoélmage.llni.gov. Mostage.llni.gov. Most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq documentation block:

LOCUG
LOCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 etGluGluMetArgGluIleArgArgLysLeuArgGluLeuGlnLeuArg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 lyAsnAsnAsnAsnAsnAsnHisAsnHisAsnHisAsnHisHisArgArg 50
                                                                                                                    Align seg 1/1 to: BG088461 from: 1 to: 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 sAspGluPheCysLeuWetPro 124
US-09-327-750D-12 x BG088461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est1:AA272375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
```

```
#81757 616 bp mRNA EST 12-SEP-1996 me95406.11 Acts amusculus convacione IMPAGE.403307 5' similar to 9b:M315.14 Shus musculus convacione IMPAGE.403307 5' similar to 9b:M3188 OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74 (HUMAN);, mRNA sequence.
                                                                                                                                     Align seg 1/1 to: AA272375 from: 1 to: 612
                                                                                                                                                                                                                                                                                                                                                                               117 sAspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                                                                                                                          526 TGATGAATTCTGCCTTATGCCT 547
                                               alignment_block:
US-09-327-750D-12 x AA272375
                                                                                                                                                                                                                                                                                                                                                                                                                                         seg_documentation_block:
LOCUS W81757
DEFINITION me95406.rl So
                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est2:W81757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nouse mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
```

Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 507. Location/Qualifiers

/organism="Mus musculus"

Source

FEATURES

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

11 (moreal)

US-09-327-750D-12 x W46041

```
us-09-327-750d-12.rst
```

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMERICALUS CHORDERS (Crandata; Vertebrata; Euteleostomi; Musmallais Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 538)
Amara, M. Hilliar, L. Allen, M., Bowles M., Dietrich, N. Dubuque, T., Geisel, S., Kucher, T., Allen, M., Bowles M., Dietrich, N. Dubuque, T., Geisel, S., Kucher, T., Le, M., Martin, J., Morris, M. Schelleberg, K., Steptoe, M., Tan, F., Undervood, K., Moore, B., Mataing, B., Mylle, T., Lennon, G., Soares, B., Milson, R. and The Mashu-HHH Mouse EST Project
Contect: Mara MyMouse EST Project
Contect: Mara MyMouse EST Project
Hashington University School of Medicinep
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Par; 314 286 1800
Email: mouseest@waten wustl.edu
Fils 1286 1800
Email: mouseest@waten wustl.edu
MAGE Consortium (info@image.lln):gov) for further information.
MGI 928806
Seq Primer mame ambiguous
High quality sequence stop: 433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS
LOCUS
DEFINITION Uselfole, y1 Sugaran moneus embryonews Mus musculus commercing
TAMGE:1466405 5' similar to gb:138189 OVARIAN GRANULOSA CELL 13.0
KD PROTEIN HGR74 (HUMAN);, mRNA sequence.
                                                                                                                                                             Align seg 1/1 to: W46041 from: 1 to: 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 saspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_estl:A1006575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
COMMENT
```

```
/db_xref-machine to the transmission of transmissi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS BE334866 542 bp mRNA EST 14-JUL-2000
DEFINITION US90A11.91 Soares_mammary_gland_NNLMG Mus musculus cDNA clone
IMAGE:3355628 5' similar to gb.#38188 OVARIAN GRANULOSA CELL 13.0
ACCESSION BE334866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 ATGGCCAATGTCCACCAGGAAAACGAAGAGAGGAGGAGCAGCCCTGCAGAA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 etGluGluMetArgGluIleArgArgLysLeuArgGluLeuGlnLeuArg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 lyAsnAsnAsnAsnAsnHisAsnHisAsnHisAsnHisHisArgArg 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetAlaAsnValHisGlnGluAsnGluGluMetGluGlnProLeuGlnAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AI006575 from: 1 to: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-327-750D-12 x AI006575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est1:BE334866.
```

11 (mouse

- - seq_name: gb_est1:A1152323

Seq_documentation_block:

LOCUS A152323 430 bp mRNA EST (30-SEP-199B)

DEFINITION Ud78402.1: Coares_mammary_gland_NMLMG MLS musculus *Commercine*
IMAGE:1477034 5' similar to qb:M39188 OVARIAN GRANULOSA CELL 13.0

ACCESSION A1152323

ACCESSION A1152323 152323.1 GI:3680792 ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Musical Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi, Manabala; Euteleria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases i to 410)
Marraw, Hillier, L. Allen, M., Bowless, M., Dietrich, M., Dubuque, T., Schellenberg, K., Sreptoe, M., Tan, F., Underwood, K., Morris, M., Pheising, B., Willer, T., Lennon, G., Soares, B., Wilson, R., and Marerston, B., Wille, T., Lennon, G., Soares, B., Wilson, R. and The WashU-HMI Mouse EST Project REFERENCE AUTHORS

TITLE JOURNAL COMMENT

Contact: Maria W/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicine
WashIngton University School of Medicine
Tel: 314 286 1810
Email: mousestedwarkson wustl.edu
This clone is available royalty/free through LLNL; contact the
IMAGE Consortium (infoelmage.llnl.gov) for further information.

Mul: 92530 Seq primer: -28ml3 rev2 Er from Amersham
High quality sequence stop: 419.
Location/Qualifiers
1. 430
Corganism-*Mas musculus*
/Ab_xet=*texon:10090*
/Aclone=*InMoSin147090*
/Aclone=*InMoSin147090*
/Aclone=*InMoSin147090*
/Alab.host=*mammary_gland_NMLMG*
/Alab.host=*mammary_gland_NMLMG*
/Alab.host=*mammary gland_/Alab.host=*minomary gland_/Alab.host=*minomary_

source

FEATURES

BASE COUNT ORIGIN

alignment_block: US-09-327-750D-12 x AII52323

Align seg 1/1 to: AI152323 from: 1 to: 430

1 MetalaAsnValHisGlnGluAsnGluGluMetGluGlnProLeuGlnAs 17

17 nGlyGluGluAspArgProValGlyGlyGlyGluGlyHisGlnProAlaG 34

seq_name: gb_est1:AW908751

seq_documentation_block:
LOCUS AM908751 503 bp mRNA EST 25-MAY-2000
DEFINITION uf57a05.y1 Scares_mammary_gland_MMLMG Mus musculus CDNA clone
IMAGE:1513440 5' similar to 99:#38188 OVARIAN GRANULOSA CELL 13.0
RD PROPEIN HGR74 (HUMAN); mRNA sequence.

AW908751 AW908751.1 GI:8073984

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Eukaryota, Matazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota, Matazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Solucognathi; Muridae; Murinae; Mus. I. (bases 1 to 503)
NCT-CGAP http://www.ncbi.nlm.nih.gov/nclcgap.
NCT-CGAP http://www.ncbi.nlm.nih.gov/nclcgap.
Tumor Gene Index Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Institute, Cancer Genome Anatomy Project (CGAP), Other-Ests: uff306; xl
Contact: Robert Straubsery, Ph.D.
Email: cgapba-Femail nih.gov
Email: cgapba-Femail nih.gov REFERENCE AUTHORS TITLE

JOURNAL

FEATURES

No.1944.29 468

No.1944.29 468

High quality sequence stop: 468

Location/Qualiflers

Actione-InfoResistations

Actione-InfoResistations

Actione-InfoResistations

Actione-InfoResistations

Actione-InfoResistations

Actione-Libe-Soares_manmary_gland_NNIMG*

Actione-Libe-Soares_manmary_gland_NNIMG*

Actione-Libe-Totales

Actione-Libe-Totales

Actione-Libe-Totales

Actione-Libe-InfoResistations

Action

/note=-vector: pr7/3D-Pac (Pharmacia) with a modified polylinker; lst efrand CDNA was prepared from mammary polylinker; lst efrand cDNA was prepared from mammary with a from a lacteting female, and was then primed with a not I collagord'y parter; boldble-stranded cDNA was lyaked to Eoo Ri adaptors (Pharmacia), digested with Not

Tue Mar 12 09:01:15 2002

```
alignment_block:
US-09-327-750D-12 x AF097440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_ro:AF187065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117. 156.

/gone-"bex;
/gone-"bex;
/gone-train-incapressed X-linked protein 3*
/product-"brain expressed X-linked protein 3*
/do_xref="ci1.46"*Aba24431.1"
/do_xref="ci1.46"*Aba24431.1"
/do_xref="ci1.46"*Aba24431.1"
/do_xref="ci1.46"*Aba24431.1"
/do_xref="ci1.46"*Aba24431.1"
/do_xref="ci1.46"*Aba24431.1"
/do_xref="ci1.46"*Aba24431.1"
/do_xref="ci1.46"*Aba24431.1"
/do_xref="ci1.46"/"
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Wetazoa: Chordata: Craniata: Vertebrata; Euteleostomi; Mammala: Eutheria: Rodentia: Sciurognathi; Muridae: Murinae; Mus. 1 (bases 1 to 85.)
Brown.A.L. and Kay.G.F.
Bexi, a gene with increased expression in parthenogenetic embryos: Hum. As member of a movel gene family on the mouse x chromosome Hum. Wol. Genet. 8 (4), 611-619 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct. 1 (1943)]

May (8(5):943)]

Day (8(5):943)]

Brown, A.L. and Kay, G.F.

Direct submission

Submitted (1960-000-1999) Cancer Unit, Queensland Institute of Medical Research, Herston RG, Brisbane, Old 4029, Australia Localion/Qualifiers

1. "St. mm." Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [[published erratum appears in Hum Mol Genet 1999]
                                                                                                  Ag097440 854 bp mRNA ROD WHO MUSCHOULUS Drain expressed X-linked protein 3 Complete cds. AF097440 GI.4580593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="near Plp"
/tissue_type="pooled organs"
/tissue_type="pooled organs"
/gene="Bex3"
172. 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             527 TGATGAATTCTGCCTTATGCCT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 sAspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seg_documentation_block:
LOCUS AF097440
DEFINITION Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seg_name: gb_ro:AF097440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.
Mus muscutus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
```

É

```
Jobses 1 to 519)
Mukal, J., Hachiya, T., Hoshino, S., Kimura, M., Nadano, D., Suvanto, P.,
Mukal, J., Hachiya, T., Hoshino, S., Kimura, M., Nadano, D., Suvanto, P.,
Direct Submission
Submitted (Jr. SEP-1999) Octolarynglogy/Pethology, Columbia
University, 630 West 168th St., Pes 11-451, New York, NY 10032, USA
1. 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus.
His dases 1 to 519)
Suvanto, P., Hachiya, F., Shoji-Hoshino, S., Kimura, M.T., Nadano, D.,
Suvanto, P., Hansaka, T., Lir, Irite, S., Greenel, L.A. and Sato, T.A.
Suvanto, P., Hansaka, T., Lir, Irite, S., Greenel, L.A. and Sato, T.A.
NADE, a pistWR-associated cell death executor, is involved in
signal transduction mediated by the common neurotrophin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Norway rat.
Katus norvegicus
Eukaryota, Aetazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mmmmalia; Eutheria; Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block: 519 bp mRNA ROD 11-JUN-2000 LOCUS AF187065 mRNA correction for not electron for action correction for many complete cds.
ACCESSION AF187065 G: 8452895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 AsnCysLeuArglleLeuMetGlyGluLeuSerAsnHisHisAspRisHi 117
                                                                                                                                                                                                                                                                                                     . Biol. Chem. 275 (23), 17566-17570 (2000)
0298829
Align seg 1/1 to: AF097440 from: 1 to: 854
```

11 (moreal

```
house mouse.

Mus muschlus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mumalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 612)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucobar, Lacy,M., Le,M., Martin,J., Mortis,M.,
Schallanderg,K., Steptec,M., Tan,P., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AA722375 612 bp mRNA EST 26-MAR-1997
DEFINITION V062407.1 Barstead mouse pooled organs MPLRB4 MMS musculus cDNA
clone IMAGE:761628 5' similar to gb:H38188 OVARIAN GRANULDSA CELL
ACCESSION AA72275 GI:1910706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Warra W/Mouse EST Project
WashurdHMI Mouse EST Project
WashurdHMI Mouse EST Project
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Teat: 314 286 1800
Pax: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 mGlyGluGluAspArgProValGlyGlyGluGlyHisGlnProalaG 34
225 TGGACAGGAACACGCCTGTGGAGAGAGTGAGGCCACACAGCAGCTGTG
                                                                                                                                                                                                                                   101 AsnCysLeuArgIleLeuMetGlyGluLeuSerAsnHisHisAspHisH1 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 GlyGlnAlaArgArgLeuAlaProAsnPheArgTrpAlaIleProAsnAr 67
                                                                             1 MetalaAsnValHisGlnGluAsnGluGluMetGluGlnProLeuGlnAs 17
                                     Align seg 1/1 to: BG088461 from: 1 to: 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                525 TGATGAATTCTGCCTTATGCCT 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 sAspGluPheCysLeuMetPro 124
US-09-327-750D-12 x BG088461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est1:AA272375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
COMMENT
```

Email: mouseest@vatson.wustl.edu This clone is available royalty-free through LLNL ; contact the TWAGE Consortium (info@image.linl.gov) for further information. %GI:462148

thmer: -28ml3 rev2 ET from Amersham quality sequence stop: 507.

1. 612 /organism-"Mus musculus"

```
/db_xref=-FVB/N*
/db_xref=-FVB/N*
/db_xref=-FAXX0:10090*
/clone=_IAbe=FAXX0:10090*
/clone=_IAbe=FAXX0:10090*
/clone=_IAbe=FAXX0:10090*
/dx=-IAbe=FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0-FAXX0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MethaksnValHisGloGluAsnGluGluMetGluGlnProLeuGlnAs 17 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 gGlnMetAsnAspGlyLeuGlyGlyAspGlyAspAspAetGluMetPhew 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AA272375 from: 1 to: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 sAspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   526 TGATGAATTCTGCCTTATGCCT 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W81757.1 GI:1392776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-327-750D-12 x AA272375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est2:W81757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
```

```
84 etGluGluMetArgGluIleArgArgLysLeuArgGluLeuGlnLeuArg 100
                                                                                                          quality sequence stop: 456.
Location/Qualifiers
1. 628
                                                                                                                                                                                                                                                                                                                                                                                                                       117 sAspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est1:AW476468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*.old
// farain="c57backfd"
// db_xref="taxon:1000"
// clone="inAcpa"; (4)330"
// clone="inAcpa"; (4)330"
// clone="inAcpa"; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; (5)320; 
alignment_scores:
Quality: 688.00 Length: .124
Quality: 5.548
Percent Similarity: 100.000 Percent Identity: 98.387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative full length read vectority overcority overcority Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 492. Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: W81757 from: 1 to: 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-327-750D-12 x W81757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Source
          ORGANISM
                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
```

```
Signature of the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organsm='Mus musculus'
/organsm='Mus musculus'
/drain='CECEH II'
/db.xef='texxon:10090'
/clone='texton:10090'
seq_documentation_block:
LOCUS AM476468 628 bp mRNA EST 24-FEB-2000
LOCUS AM476468 1 NOL CGAP_LDJ3 Mus musculus cDNA clone IMAGE:2937027 5'
DEFINITION UG/76402.1' NOL CGAP_LDJ3 Mus musculus cDNA clone IMAGE:2937027 5'
similar to qb:M38188 OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74
(HUMANN); mRNA sequence.
ACCESSION AM476468.1 GI:7046574
```

1 others

93 t

172 g

157 c

162 a

```
us-09-327-750d-12.rst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bouse mouse.

Was masculus
Bukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryots, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bassa 1 to 585)
NCT-CGAP http://www.ncbi.nlm.nih.gov/nctcgap.
NRT-CGAP fittp://www.ncbi.nlm.nih.gov/nctcgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index.
(Uppublished (1997)
(Optoct: Robert Strausberg, Ph.D.
Enail: Gapbar Strausberg, Ph.D.
Enail: Gapbar Strauslable royalty-free through LLNL; contact the RAKGE Consortlum (info@mage.llnl.gov) for further information.
                                                                                                                                17 nGlyGuGuApArgProValGlyGlyGlyGlyGlyGlyHsGlnProAlaG 34
191 rGsACAGAACGCCCTGGGGAGAGATGACCTCTG 240
191 rGsACAGAACGCCCCTGGGAGAGAGATGAGGCTCACAGCTGCTG 240
                                                                                                                                                                                                                                                                                               101 AsnCysLeuArgIleLeuMetGlyGluLeuSerAsnHisHisAspHisHi 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 ATGCCCAATGTCCACCAGGAAACGAAGAGATGGAGCAGCCCCTGCAGAA 190
                                                                                                                                                                                                       34 lyAsnAsnAsnAsnAsnAsnHisAsnHisAsnHisAsnHisHlsArgArg 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -40RP from Gibco
High quality sequence stop: 465.
Location/Qualifiers
1. :885.
Cogranism="Mus musculus"
/Ab_xref="texon:10090"
/Clone="IMAGE:3255677"
/Clone="IMAGE:3255677"
/fissue_type="manmary_gland_NNLMG"
/fissue_type="manmary_gland"
/lab_host="PHIUS"
                                                                                                                                                                                                                                                                          51 GlyGlnAlaArgArgLeuAlaProAsnPheArgTrpAlaIleProAsnAr 67
Tue Mar 12 09:01:17 2002 (6)(b)
                                                                  mores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 sAspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_estl:BE334877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS BE334877
DEFINITION us90b10.y1 So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
```

```
Muse mouse.

Mus musculus

Bukaryota, Retazoa, Chordata, Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musina.

Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schallenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B.,

Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Washu-HHMI Mouse EST Project
Onpublished (1996)
Conteact: Marra W./Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Froest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                      166 ATGGCCAATGTCCACCAGGAAAACGAAGAGATGGAGCAGCCCTGCAGAA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 etGluGluMetArgGluIleArgArgLysLeuArgGluLeuGlnLeuArg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 AsnCysLeuArgIleLeuMetGlyGluLeuSerAsnHisHisAspHisHi 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466 AATTGTCTACGCATCCTTATGGGGGAGCTGTCTAACCACCACGATGATCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                     17 nGlyGluGluAspArgProValGlyGlyGlyGluGlyHisGlnProAlaG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 lyAsnAsnAsnAsnAsnAsnHisAsnHisAsnHisAsnHisHisArgArg 50
                                                                                                                                                                                                                                                                                                                                            1 MetAlaAsnValHisGlnGluAsnGluGluMetGluGlnProLeuGlnAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #64711 590 bp mRNA EST M64711 14.5) colore Library MSE3.1 Sources mouse embryo NDME13.5 14.5) colore Library 87.5 similar to qb:W38188 OWI 13.0 KD PROTEIN HGR74 (HUMAN);, mRNA sequence
                                                                                                                        Quality: 688.00 Length: 124
Satio: 5.546 Gaps: 90.00
Percent Similarity: 100.000 Percent Identity: 98.387
                                                                                                                                                                                                                                                                                          Align seg 1/1 to: BE334877 from: 1 to: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W64711
W64711.1 GI:1372353
                                                                                                                                                                                                                    alignment_block:
US-09-327-750D-12 x BE334877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS W64711
DEFINITION md71g01.rl So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_est2:W64711
                                                                                                  alignment_scores:
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anote—"Vector: pf773D-Pac (Pharmacia) with a modified polylinker; ist strand cobw was prepared from ammary and tissue from a lactating female, and was then primed and tissue from a lactating female, and was then primed with a Not I - ollgo(df) primer. Double-stranded CDNs was ligated to Eon RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pp713 vector. Library is normalized Library was constructed by Bento Soares and W. Fathma Bonaldo.
```

```
Albanates (Anote-Vector pSPORTI; Site_1: Sall; Site_2: NOLI; This clone is among a rearrayed set of 15.24 clones from 11 metry of the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "curei_cals: naisouv.-3
Laboratti George J. Kargul
Laboratory of Genetics
Wetional Institute on Ading/National Institutes of Health
National Institute on Ading/National Institutes of Senetics
Bmail conselgau. Strine 4000, Baltimore, ND 2122-6630, USA
Email conselgau. Strine 4000, Baltimore, ND 2122-6630, USA
Plai clone set has been freely distributed to the community. Please
Visit http://dsun.prc.nia.nih.gov/CDNA/15k.html for details.
Seq primer: -21M13 Reverse
High quality sequence stop: 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Musual mouse.

Musual material and detazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mamabla; Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases I to 599)

7. (bases I to 59)

7. S.; Carter, M.; Oldan, Y., Lim, M.K., Jaradat, S.A., Tanaka

7. S.; Carter, M.; and Ro, M. S.H.; Oldan, Y., Clim, M.K., Jaradat, S.A., Tanaka

Verification and initial annotation of NIA mouse 15K CDNA clone set Unpublished (2001).
                                                                                                                                                                                             Seg_documentation_block:
LCCUS
LCCUS
BG088461 599 bp mRNA EST 26-JAN-2001
DEFINITION H3153D07-5 NIA Mouse 15K CDRA Clone Set Mus musculus CDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Ocganism="Mus musculus"
/strain=C5PM.63-
/db.xref=traxon:10090*
/clone=#13151900*
/clone=#13151900*
/strain=#13151900*
/strain=#13151900*
/strain=#13151900*
/strain=#13151900*
/strain=#131690*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores;
Quality: 688.00 Length: 124
Ratio: 5.548 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .599
                                  484 TGATGAATTCTGCCTTATGCCT 505
                                                                                                                                                                                                                                                                                                                                                                        BG088461
BG088461.1 GI:12571025
                                                                                                                                             seq_name: gb_est2:BG088461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163
                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
34 lyAsaAsaAsaAsaAsaAsaHisAsaHisAsaHisAsaHisHisArgArg 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 etGluGluMetArgGluIleArgArgLysLeuArgGluLeuGlnLeuArg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: W64711 from: 1 to: 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 sAspGluPheCysLeuMetPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-327-750D-12 x W64711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                FEATURES
```

alignment_block:

Run on:

```
Human brain expressions with a secreted profusers of the secreted prof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New p75-neurotrophin receptor associated cell death executor (NADE) and
the gene encoding NADE, useful for medulating the activity of p75NTR
and for detecting neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurotrophin receptor; p75-NTR; NGF-induced apoptosis; neurogenetic disease; NF-kappaB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Fig 1; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
AAF23528
ID AAF23528 standard; DNA; 700 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UMEO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-2000; 2000WO-US15621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1999; 99US-0327750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-061707/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200075278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse NADE DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-DEC-2000.
           AAF23528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
               Mouse NADE DNA. H
Human shorest and o
Human secreted pro
Human secreted pro
Human secreted pro
Ruman ovarian tumo
Human cDNA clone (
Human cDNA sequenc
CDNA encoding CDIF
Human secreted pro
                                                                                                                                                                                                                       March 11, 2002, 15:42:51; Search time 144 Seconds (Without alignments) 4467:593 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.
                                                                                                                                                                                                                                                                                                                                              US-09-327-750D-28
700
1 a Ogagegtctggccagcagc......gggggcttgtgtgccagtga 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | N_Genese_1101:*
| SIDSZ/godata/geneseq/geneseqn/NA1980.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1980.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1980.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1980.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1981.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1981.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1981.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1981.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1981.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1991.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1991.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1991.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1991.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1991.DAT:*
| SIDSZ/godata/geneseq/geneseqn/NA1991.DAT:*
| SIDSZ/godata/geneseq-geneseqn/NA1991.DAT:*
                                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         930621 seqs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        693.6

693.6

693.6

100.2

115.7

115.7

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

115.8

11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Score Match 1
                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score;
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
```

Page

3;

Gapa

```
Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                             431 ggagatgagagatccggagagaagcttagggagctacagctgagaaattgtctacgcat 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                506 ggagatgagagaaatcagaagaaaacttagggagctgcagttgaggaattgtctgcgtat 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                611 attttcctgacatgcctttaatgacccgtttgtggtgagccctgtgttatttccatgcca 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               685 attttcctaatatgcctttactgatccgtttgctgtgaaccctatgttattt----cca 739
                                                                            Query Match
40.74; Score 284.6; DB 21; Length 917;
Best Local Similarity 78.54; Pred; No. 3.4e-69;
Matches 399; Conservative 0; Mismatches 64; Indels 45;
  cerebral anoxia and epilepsy; and infectious diseases.
                              Sequence 917 BP; 228 A; 203 C; 270 G; 211 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein 5' EST, SEQ ID No: 1003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACO1005 standard, CDNA, 532 BP.

ACO1005;

ACO-007-000 (first entry)

XX

ACO1005;

XX

Bunan secreted protain 5' EST. SEQ

XX

Human; 5' EST. expressed sequence t

XX

Human; 5' EST. expressed sequence t

XX

Human; 6' EST. expressed sequence t

XX

Human; 6' EST. expressed sequence t

XX

CS

Homo sapiens.

XX

CSEP-2000.

PR

2-FEB-2000; 2000EP-0200610.

PR

2-FEB-1999; 99US-0122487.

XX

CEST ) GENSET.

Dumas Milne Edwards J, Duclert A,

XX

XX
  ខ្លួន
                                                                                                                                                                                                                                               셤
                                                                                                                                                                             g
                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                          8 8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAF21614 - AAF22031 represent DNA sequences encoding human propretains AAF26711 - AAF22031 represent DNA sequences are associated with breast and oversion cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the sequences AAF22032 - AAF22040 and AAB59129 which are used in the invention and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; municosupressive; nootropic; neuroprotective; antititization; antitionamic protein sequences or intition and protein sequences are used in the diagnosis of cancer, polityuchectide and protein sequences are used in the diagnosis of cancer, prevention and treatment of immune absorders e.g. Addison's disease, allergies, autofimmune hemolytic anaemia, autofimmune thyroiditis, diabetes mellitus, crohn's disease, allergies, autofimmune hemolytic anaemia, autofimmune thyroiditis, diabetes mellitus, crohn's disease, allergies, autofimune hemolytic anaemia, autofimune thyroiditis, arthuista and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as
                                                                                                                                                                                                                                                                                                                                                               Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; motorropic, neurpprotective, antivitai, antializerjc; hepartotropic; antidiabetic; antidicabetic; antidicabetic; antidicabetic; antidicabetic; antidicabetic; antidicatic; cardant; immune disorder; antibotectis, anticonvolsant antibotectingal; antiparastic; cardant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anamia autoimmune thyroiditis; diabetes mellitus; crobn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; vound healing; neurological disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and disapposis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
Human breast and ovarian cancer associated antigen gene SEQ ID 135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 581-582; 1299pp; English.
                                                                                                                                                                                                                               AAF21748 standard; DNA; 917 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2000; 2000WO-US05881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1999; 99US-0124270.
                                                                                                                                                                                                                                                                                                    27-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-611515/58.
P-PSDB; AAB58845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA, Ruben SM;
                                                                                                               689 tgttgccag 697
                                                                                                                                   WO200055173-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000,
                                                                                                                                                                                                                                                                   AAF21748;
                                                                                                                                                                                                                                    ò
                                                                               a
                                                                                                             ò
                                                                                                                                              9
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel ovarian tumor proteins, and nucleic acids encoding them, used to treat and diagnose cancers, particularly ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH82377 to AAH83878 represent human ovarian tumour-associated polynucleotide sequences which encode ovarian tumour proteins. The ovarian tumour protein and polynucleotide sequences have cytostatic activity, and can be used in gene therapy and vaccine production. The ovarian tumour proteins and polynucleotides can be used to inhibit the development of cancer, particularly ovarian cancer. They can also be used to diagnose the onset and progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ovarian tumour associated polynucleotide sequence SEQ ID NO:210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Indels 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      636 cogrttgraggraggccctgtgttattccatgccatgtgccaggtggggcttggt 691
179 cognttgratgaaccctatgctatt------catgcgtaaatgggcttggt 228
                                                                                                                                          Human; ovarian tumour; ovarian cancer; diagnosis; gene therapy; Immunogenic; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 18.2%; Score 127.2; DB 22; Length 426; Best Local Similarity 79.7%; Preci No. 11e-25; Marches 18; Conservative 0; Mismatches 40; Indels 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 426 BP; 86 A; 106 C; 90 G; 137 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA clone (5'-primer) SEQ ID NO:352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 100; 338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH03517 standard; cDNA; 865 BP.
AAH82586 standard; cDNA; 426 BP.
                                                                                                                                                                                                                                                                                                                  16-JAN-2001; 2001WO-US01575.
                                                                                                                                                                                                                                                                                                                                                    14-JAN-2000; 2000US-0176722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2001 (first entry)
                                                                       25-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-425866/45.
                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                          WO200151513-A2.
                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                             19-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                              Algate PA;
                                     AAH82586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAB7080 to AAAB7656 represent nucleic acid sequences (NI) encoding a accrinogenesis biomarkers. The actrinogenesis biomarkers are induced by treating ret heptocytes with phenobarbitol. The nucleic acids are acid set in feptocytes with phenobarbitol. The nucleic acids are can be used to derive probes and/or primers for detecting or inducing carcinogenesis, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 getetetaateaccacgaccatcacgatgaattetgeettatgeettgaetteggteatt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503 getgtetaaccaccacgatcaccatgatgaattetgeettatgeettgaetteggteatt 562
                                                                                                                                                                                                                                                                             Rat; phenobarbitol; carcinogenesis marker; carcinogenesis; detection; identification; carcinogenic; probe; primer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding a carcinogenic biomarker, induced by membarbitol ireament of rac hepatocytes, useful for identifying carcinogenic compounds -
                                                                                                                                                                                                                                          Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 21.0%; Score 147.2; DB 21; Length 187; Best Local Similarity 69;4%; Pered: No. 214-31; Metches 169; Conservative 0; Mismatches 18; Indels 1; Matches 169; Conservative 0; Mismatches 18; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 187 BP; 39 A; 48 C; 40 G; 60 T; 0 other;
    Bunch RT, Curtis SW, Rodi CP, Morris DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 73; 240pp; English.
                                                                                                                             AAA87147 standard; DNA; 187 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JAN-2000; 2000WO-US00503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-1999; 99US-0118078.
                                                                                                                                                                                                          08-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SEAR ) SEARLE & CO G D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-505977/45.
                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         623 tgccttta 630
|||||||||
180 tgccttta 187
                                                                                                                                                                                                                                                                                                                                                                             WO200044902-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000.
                                                                                                                                                                       AAA87147;
```

RESULT AAH82586

g

ò

g ò 22-MAR-2001.

```
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ç
                                                                                                                                                                        ÷
the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cONAs. The primers are also useful for the detection and/or disgnosis of the abnormality of the proteins encoded by the full-length cONAs. The primers allow obtaining of the full-length ADMSs. The primers allow obtaining of the full-length ADMSs. The primers allow obtaining of the full-length ADMSs. The present human cDNA sequences; ADMS246 to ADMSS33 represent human cDNA sequences; ADMS246 to are represent oligonuclectides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                           203 agagciggagcag...eccctgcagaatggacaggaacaccgcccttgggaggaggtga 259
256 aggagggaggcccccacagcagaataagaagaatccccgccattgggaggggggg 315
                                                                                                                                                                                                                                                                           316 aggccagaagcctggaggaaatatca----- 341
                                                                                                                                                                                                                                                                                                                  320 ccgaagaggcaaggtcagcgacctgccctaacttccgatgggccattcccaacaggca 379
342 --ggcggggcagttaggcgactgccctaatttcgatgggcaacacctaataggca 399
                                                                                                                                                                                                                                                                                                                                                             380 gatgaatgacgggttgggtggagatggagatgatatggaaatgttcatggaggagatgag 439
                                                                                                                                                                                                                                                                                                                                                                           440 agagatocgggagaaagcttagggagctacagctgagaaattgtctacgcatocttatggg 499
                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 11.5%; Score 80.2; DB 22; Length 1229; Best Local Similarity 56.2%; Pred. no. 1.8-12; Marches 269; Conservative 0; Mismatches 159; Indels 57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        560 attececetgagatecatactgtgactecegetgtageettteeetegeatitteet 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human: cell differentiation; CDIFF; agonist: antagonist; epilepsy; cell proliferation; Alzheims' dileases; cantipophrenic disorder; arteriosclerosis; dancer; athorosclerosis; diabetes mellitus; ss.
                                                                                                                   Seguence 1229 BP; 351 A; 243 C; 296 G; 339 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding CDIFF-4, Incyte ID No. 1990956CB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
250..612
/*tag* a
/product= "CDIFF-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC85548 standard; cDNA; 1364 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200119860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC85548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               888888888888
                                                                                                                                                                                             à
                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                      9 9 9 9
                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                        03
03
03
                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            유
                                                                                                                                                                                                                                  ò
```

```
The sequences given in AAC85545-72 encode human polypeptides involved to the sequences given in AAC85545-72 encode human polypeptides and agonists of these are used to treat a disease or condition associated with decreased expression of functional loster. A mategorist of CDIFF is decreased expression of functional loster of CDIFF is condition associated with over expression of functional loster. CDIFF polypeptides may be used for the treatment, confunction and disporders, supplyeptides may be used for the treatment, conversion and disporders, and a Alianders and sequence is homologous to Man musculus and expression are policysy. The CDIFF-4 sequence is homologous to Man musculus and playsy. The CDIFF-4 sequence is homologous to Man musculus in 157.4 to 158 0 centimorgans, to chromosome 3 within the interval from from 104.2 to 156.0 centimorgans and to the X chromosome within the interval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 gatgaatgacgggttgggtggggatggagatgatatggaaatgttcatggaggatgag 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459 tattgagcacaa-----tgaagcgagagatgatgtagaaaaggtttgtagggcagatgat 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 goccagaatagoaaccaggaaacaaaatotoatogoccaatgtocaccaggaaacga 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 gggccaccagcctgctgcaaacaacaacaacaacaccacataaccacacaccaca 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 agagateeggagaaagettaagggagetacagetgagaaattgtetaegeateettatggg 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 11.5%; Score 80.2; DB 22; Length 1364; Best Local Similarity 56.2%; Pred. No. 1.8-12; Matches 769; Conservative 9; Mismatches 159; Indels 57; Gaps
                                                                                                                                                                                                            Hillman JL, Yue H, Reddy R, Lal P, Shah P, Azimzai Y; , Lu DAM, Bandman O, Shih LL, Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptides and polynucleotides involved in cell differentiation are used for treatment, prevention and diagnosis of cell proliferative, developmental and neurological disorders e.g. cancer and Albehmer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1364 BP; 411 A; 269 C; 322 G; 362 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 121; 137pp; English.
                                                             15-SEP-1999; 99US-0154140.
06-DEC-1999; 99US-0169155.
                                                                                                                                                       (INCY-) INCYTE GENOMICS INC.
14-SEP-2000; 2000WO-US25435.
                                                                                                                                                                                                                                                                                                          WPI; 2001-211447/21.
P-PSDB; AAB47126.
                                                                                                                                                                                                                    Tang YT, Hi
Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
```

```
Human cell cycle and proliferation proteins and polynucleotides are used to treat, dispanse and prevent immune, developmental and cell signaling disporders and cell proliferative disorders including cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillman JL, Lal P, Tang YT, Yue H, Au-Young J, Bandman O; Azimzai Y, Yang J, Lu DAM, Baughn MR, Patterson C, Shah P;
Cell cycle and proliferation protein; CCYPR; human; agonist; antagonist; gene therapy; detection; gene therapy; transgenic animal disease model; immune disorder; transgenic animal disorder; cell signaliniq disorder; cell proliferative disorder; cancer; tumour; anamia; epilepi atterioscierasis; asthma; alleray; disbeces melitus; menstrual cycle disorder; bacterial infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 181-182; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                    99US-0145075.
99US-0153129.
99US-0164647.
                                                                                                                                                                                                                                                                                                                          21-JUL-2000; 2000WO-US19948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-112727/12.
P-PSDB; AAB60474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetes mellitus, caused by bacteria.
                                                                                                                                                                                                                               W0200107471-A2.
                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1999;
08-SEP-1999;
10-NOV-1999;
                                                                                                                                                                                                                                                                             01-FEB-2001.
      NAME OF THE PROOF THE PROO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the coding sequence for human X chromosome linked there expression protein in 14. The protein and coding sequence are useful for treating diseases e.g. cancer and HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cell cycle and proliferation protein CCYPR-22 cDNA, SEQ ID NO:76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 accaccgaagagccaggctcgccgacctgccctaacttccgatgggccattcccaaca 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 tgagagagatccggagaaagcttagggagctacagctgagaaattgtctacgcatcctta 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496 tggggggagetgtetaaceaecaecaecatgatgatgattetgeettatgeettgaette 555
                                                                                          Human X chromosome linked gene expression protein 14 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 accgtaggcggttccgcgttaggcagccatctgcagtatagatgggacataatgcata 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 ggcagatgaatgacgggttgggtggagatggagatgatatggaaatgttcatggaggaga 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 geactgatececet -- caccatgaccateaegatgagttttgcettatgeetgaatee 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptide-human X chromosome linked gene expression protein 14 and polynucleotide for coding said polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                     Human; X chromosome linked gene expression protein 14; cancer; HIV infection; cytostatic; anti-HIV; chromosome X; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

8.0%; Score 55.8; DB 22; Length 767;
Best Local Similarity 53.7%; Pred No. 84e-06;
Maches 139; Conservative 0; Mismatches 117; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 767 BP; 224 A; 143 C; 215 G; 185 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 24 (Disclosure); 31pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (SHAN-) SHANGHAI BORONG GENE DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF59611 standard; cDNA; 898 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              556 ggtcattccccctgagat 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 tgatggtttccctgaagtt 510
                                                                                                                                                                                                                                                                                                                                            23-NOV-1999; 99CN-0124078.
                                                                                                                                                                                                                                                                                                                                                                                         99CN-0124078.
                                             17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483897/53.
P-PSDB; AAG66407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mao Y, Xle Y;
                                                                                                                                                                                                          Homo saptens.
                                                                                                                                                                                                                                                                                                                                                                                         23-NOV-1999;
                                                                                                                                                                                                                                                                                               30-MAY-2001.
                                                                                                                                                                                                                                                    CN1296969-A.
      AAH75810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF59611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
AAF59611
ID AAF
XX
AC AAF
XX
DT 24-1
XX
XX
XX
XX
      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
```

```
cell cycle and proliferation proteins (CYPR) ABBG053-ABB0506.

Cell cycle and proliferation proteins (CYPR) ABBG056.

CCTPR and agonists of CCTPR are used to treat diseases or conditions
associated with decreased expression of functional CCTPR, while CCTPR
antagonists are used to treat diseases or conditions associated with
Overexpression of functional CCTPR. Monocloan or polycloan antibodies

CC confoundments are used to treat diseases or conditions associated with
Overexpression of functional CCTPR. Monocloan or polycloan antibodies

CC compounds est, antibodies oligionuclectides and proteins (receptors)
that specifically bind to CCTPR, and in drug screening methods to
incledides can be used to generate transgenic animal models of human
disease, and can be used to generate transgenic animal models of human
disease, and can be used to generate transgenic animal models of human
disease, and can be used to generate transgenic animal models of human
disease, and can be used to generate transgenic animal models of human
disease, and can be used to generate transgenic animal models of human
diseases which can be used to generate aspectated with CCTPR.

CC Diseases which can be diagnosed, treated and prevented using CCTPR
proteins, nucled calds, agonists or antagonists include immune,
discoders including cancer. Specific examples of these discreters
classforces including cancer. Specific examples of these discreters
classforces include annema, epilepsy, arteriosolerosis, asthma, cancer, allergies,
clabels are mediated the menstrual cycle and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 accaccgaagagccaggctcgccctcaacttccgatgggccattcccaaca 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 ggcagatgaatgacgggttgggtggagatggagatgatatggaaatgtcatggaggaga 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436 tgagagagatccggagaaagcttagggagctacagctgagaaattgtctacgcatcctta 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match

8.0%; Score 55.8; DB 22; Length 898;
Best Local Similarity 53.7%; Pred. No. 98-06;
Matches 139; Conservative 0; Mismatches 117; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 898 BP; 250 A; 186 C; 251 G; 211 T; 0 other;
```

Run on:

```
Human cell; cycle a Human cell; cycle a Human polymucleott Human polymucleott Human polymucleott Human secreted pro Human secreted pro Human secreted pro Oligonucleottde Di Human secreted pro Probe # Alls & used t Human polymucleottde Human polymucleottde Human polymucleottde Human polymucleottde Human polymucleottde Human polymucleott Human polymucleott Human colon cencer Human polymucleott Bunan polymucleott Human polymucleott Bunan Buna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New p75-neurotrophin receptor-associated cell death executor (NADE) and
the gene encoding NADE, useful for modulating the activity of p75NTR
and for detecting neurodegenerative diseases
      brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neurotrophi: receptor; p75-NTB; NGF-induced apoptosis; neurogenetic disease; NF-KappaB; ds.
AMF5611
AMF5611
AMF5611
AMF5610
AMF5610
AMF66105
AMF66105
AMF66105
AMF6825
AMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF23529 standard; DNA; 891 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-2000; 2000WO-US15621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .02-7UN-1999; 99US-0327750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-2001 (first entry)
2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-061707/07.
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
411110000
41110000
41110000
41110000
41110000
41110000
41110000
41110000
41110000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
4111000
411000
411000
411000
411000
411000
411000
411000
411000
411000
411000
411000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
41000
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200075278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human NADE FWA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapie:s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF23529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sato Ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NADE DNA. H
Human Dresst and o
Human Secreted pro
Mouse NADE DNA. M
Human secreted pro
Human ovarian tumo
Human open signatu
Ruman CDNA clone (
Human CDNA clone (
Human CDNA clone (
                                                                                                                                                                                                                                                                                                                                                 March 11, 2002, 16:36:39; Search time 144 Seconds
(Walhout alignments)
5304.700 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-327-750D-29
891
1 arcceatcocceattcotat......aataaagcaatttaaaaagc 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N. Geneseq_1101:*

1. $IDS2/gcdata.geneseq/geneseqn/NA188. DAT:*

2. $IDS2/gcdata.geneseq/geneseqn/NA188. DAT:*

4. $IDS2/gcdata.geneseq-geneseqn/NA188. DAT:*

5. $IDS2/gcdata.geneseq-geneseqn/NA188. DAT:*

5. $IDS2/gcdata.geneseq-geneseqn/NA189. DAT:*

5. $IDS2/gcdata.geneseq-geneseqn/NA189. DAT:*

7. $IDS2/gcdata.geneseq-geneseqn/NA189. DAT:*

8. $IDS2/gcdata.geneseq-geneseqn/NA189. DAT:*

9. $IDS2/gcdata.geneseq-geneseqn/NA189. DAT:*

10. $IDS2/gcdata.geneseq-geneseqn/NA189. DAT:*

11. $IDS2/gcdata.geneseq-geneseqn/NA199. DAT:*

12. $IDS2/gcdata.geneseq-geneseqn/NA199. DAT:*

13. $IDS2/gcdata.geneseq-geneseqn/NA199. DAT:*

14. $IDS2/gcdata.geneseq-geneseqn/NA199. DAT:*

15. $IDS2/gcdata.geneseq-geneseqn/NA199. DAT:*

16. $IDS2/gcdata.geneseq-geneseqn/NA199. DAT:*

17. $IDS2/gcdata.geneseq-geneseqn/NA199. DAT:*

18. $IDS2/gcdata.geneseq-geneseqn/NA199. DAT:*

19. $IDS2/gcdata.geneseq-geneseqn/NA199. DAT:*

11. $IDS2/gcgdata.geneseqn/NA199. DAT:*

12. $IDS2/gcgdata.geneseqn/NA199. DAT:*

23. $IDS2/gcgdata.geneseqn/NA199. DAT:*

24. $IDS2/gcgdata.geneseqn/NA199. DAT:*

25. $IDS2/gcgdata.geneseqn/NA199. DAT:*

27. $IDS2/gcgdata.geneseqn/NA199. DAT:*

28. $IDS2/gcgdata.geneseqn/NA199. DAT:*

29. $IDS2/gcgdata.geneseqn/NA199. DAT:*

21. $IDS2/gcgdata.geneseqn/NA199. DAT:*

22. $IDS2/gcgdata.geneseqn/NA199. DAT:*

22. $IDS2/gcgdata.geneseqn/RA199. DAT:*

22. $IDS2/gcgdata.geneseqn/RA199. DAT:*

22. $IDS2/gcgdata.geneseqn/RA199. DAT:*

22. $IDS2/gcgdata.genesequ/geneseqn/NA199. DAT:*

22. $IDS2/gcgdata.genesequ/geneseqn/NA199. DAT:*

22. $IDS2/gcgdata.genesequ/geneseqn/RA199. DAT:*

23. $IDS2/gcgdata.genesequ/genesequ/RA199. DAT:*

24. $IDS2/gcgdata.genesequ/genesequ/RA199. DAT:*

25. $IDS2/gcgdata.genesequ/genesequ/RA199. DAT:*

26. $IDS2/gcgdata.genesequ/genesequ/RA199. DAT:*

27. $IDS2/gcgdata.genesequ/genesequ/genesequ/RA199. DAT:*

27. $IDS2/gcgdata.genesequ/genesequ/genesequ/RA199. DAT:*
                                                                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      930621 segs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 04
Maximum Match 1004
Listing first 45 summaries
                                                                                                                                                                                                                                                                  · nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score Match Let

889.4

889.4

564.4

564.4

564.4

564.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4

566.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                score:
                                                                                                                                                                                                                                                                  OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect sc
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
```

```
The present sequence is one of a large number of 5' ESTs derived from canna encoding secreted proteins. An ORP has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs or polyA+ RNAs or polyA+ RNAs or polyA+ CATS of ESTs were set asually correspond an anny to the 3' untranslated region (UTR) of the mRNA because they are often otherhed from oilgo-dryptimed chank librates. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of the mRNAs and even in those cases where longer cDNA sequences have been obtained; the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intent f' ends and can therefore be used to obtain full length contained. The full 5' UTR is rarely included. 5' ESTs are derived from mRNAs and genomic DNAs. 8' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain cutting contain wetches. They are used to obtain we vectors.
                                                                                                                                                                                                                                                                                                      28) aqaanaaccagcagaanaaaaaactctcatcatggcaaatattcaccaggaaaagga 340
188 agaanaacaggaaaaaaaatctcatcatggcaaatattcaccaggaaaaggaaagg 247
                                                                                                                                                                                                                                                                                                                                              401 ccagoctgcaggaaatcgacggggacaggctcgccgacttgcccctaattttcgatgggc 460
                                                                                                                                                                                                                                                                                   Gaps
New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining chans and genoulc DNAs that correspond to 5'ESTs and for diagnostic, forestic, gene thatapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                   0; Indels 0;
                                                                                                                                                                                                                                                            Ouery Match 38.5%; Score 343; DB 21; Length 532; Best Local Similarity 98.6%; Pred. No. 66-93; Marches 340; Conservative 5; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurotrophin receptor; p75-NTR; NGF-induced apoptosis; neurogenetic disease; NF-kappaB; ds.
                                                                                                                                                                                                                                Sequence 532 BP; 151 A; 121 C; 163 G; 91 T; 6 other;
                                            Claim 1; SEQ ID 1003; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                          ç
                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                           326 ccaggaaaacgaaqagatgagcagcctatgcagaatggagagagaagaccgcctttggg 385
                                                                ctttgcactcagtgtaagtttctgtcagcagtagtttcacccatttgcatggaaaattt 865
                                                                                                                                                                                                                                                                                                                                                                                      305 ccaggaaaacgaagagatggagcagcctatgcagaatggagaggaagaccgccctttggg 364
    0; Gaps
    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein 5' EST, SEQ ID NO: 1003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dumas Milne Edwards J, Duclert A, Giordano J;
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   866 aaagccaataaagcaatttaaaaagc 891
                                                                                                                                                                                                                                                                                                                                                                                                                                       845 aaagctaataaagcaatttaaaaagc 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
AAC01005
LD AAC01005 standard; cDNA; 532
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1999; 99US-0122487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-OCT-2000 (first entry)
    Matches 565; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-500381/45.
P-PSDB; AAG00999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC01005;
                                                                                                           446
                                                                                                                               425
                                                                                                                                                                                                                                                                                                                                                                         908
                           ģ
                                                                                      8 8 8
                                                                                                                                                  6 6 6 6 6
                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                      đ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                ò
```

S

à a

```
A single-stranded DNA (or its complementary strand or the corresp. Co double-stranded DNA) which comprises one of the 7837 'GS' sequences of quent in AAT19001-72687 and which is able to hybridise to part of given in AAT19001-72687 and which is able to hybridise to part of complement DNA, cDNA or make is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed onthe libraries prepared from the complement of the property of the particular walks specified and bundance of the appearance frequency of a given GS in a onstructuded so as to reflect accurately the relative abundance of the appearance frequency of a given GS in a obtain it was desired. The appearance frequency of a given GS in a obtain it was desired. The appearance frequency of a given GS in a obtain it was desired. The appearance frequency of a given GS in a constructude of the primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       788 cttctatttgaagattgcctttgcactcagtgtaagtttctgtcagcagtagtttcacce 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying gene signatures in 3'-directed human cDNA library - e.g. for disgnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human Lissues
                                                                                                                                                                                                                                                                                                                 Gene signature; messenger RNA; mRNA; relative abundance; frequency;
human, cloning; mapping; non-bissed library; diagnosis; detection;
cell typing; aboramal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 98.8%; Pred. No. 1.7e-38;
Matches 162; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 169 BP; 47 A; 30 C; 34 G; 58 T; 0 other;
                                                                                                                     RESULT 7
ANT21034
1D AAT21034 standard; cDNA to mRNA; 169 BP.
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 786; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                 Human gene signature HUMGS02316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-NOV-1994; 94WO-JP01916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1993; 93JP-0355504.
                                                                                                                                                                                                                                         03-JUL-1996 (first entry)
                     Matsubara K, Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                          W09514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1995.
                                                                                                                                                                                                   AAT21034;
                                                        8
                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel ovarian tumor proteins, and nucleic acids encoding them, used to treat and diagnose cancers, particularly ovarian cancer -
                                                                                                                                                                                                                                                              Human ovarian tumour associated polynucleotide sequence SEQ ID No:210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM82377 to AAM83878 represent human ovarian tumour-associated polynucleotide sequences which encode ovarian tumour proteins. The ovarian tumour protein and polynucleotide sequences have cytostatic activity, and can be used in gene therapy and vectoria protein. The ovarian tumour proteins and polynucleotides can be used to disciplinity the development of cancer, particularly ovarian anner. They can also be used to dispose the onset and progression of cancer. They can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           791 ctattigaagatigocittigoacteagigtaagittotgicagoagigagittoacocatt 850
239 ctattigagatigocittigaattoagigtaagittotgicagoaatagittoaocoatt 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 30.7%; Score 273.8; DB 22; Length 426; Best Local Similarity 97:8%; Pred. No. 3.2e-75; Indels 3; Gaps Matches 308; Conservative 0; Mismatches 5; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                 Human; ovarian tumour; ovarian cancer; diagnosis; gene therapy; immunogenic; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 426 BP; 86 A; 106 C; 90 G; 137 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 100; 338pp; English.
                                                                                                                                              AAH82586 standard; cDNA; 426 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JAN-2001; 2001WO-US01575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-2000; 2000US-0176722.
                                                                                                                                                                                                                           25-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-425866/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                          WO200151513-A2.
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Algate PA;
                                                                                                                                                                                      AAH82586;
```

ò

a

ŏ QQ ŏ a

6 6 6

ö

2; Indels 0; Gaps

ço Go

```
complementary strand of a polynuclectide which comprises a 5'-end sequence and an oligonuclectide comprising a sequence complementary to a complementary and sequence and an oligonuclectide comprises a 3'-end sequence, where the polynuclectide which comprises a 3'-end sequence, where the compination of coligonuclectide comprises at least 15 nuclectides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for sphtebalship polynuclectides, contained to particularly full-length conka. The primers are also useful for the detection and/ord disgnosis of the abnormality of the proteins encoded by contained to Ahilb'12 represent them conka sequences; Ahilb'12 and Ahilb'12 represent human amino and sequences; Ahilb'12 to Ahilb'12 represent human amino and sequences; and Ahilb'22 to Ahilb'22 to the present the present three is all of which are used in the exemplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            517 tattcatggagagaqatgagagaaatcagaaqaaaacttagggagctgcagttgaggaatt 576
435 ggtttgraggcaggtcggtggtggaaatcaagagaaagataggaacaggaagagaggact 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 aaasacaaccagaaaaaaaaaaatctcatcgcaaatattcaccaggaaaacgaagaga 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 aagaggaactagcggcaaacatctcaacggggaaaatgcccaacaagaaaacgaaggag 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           457 gggccatacccaataggcagatcaatgatgggatgggtggagatggagatgatatggaaa 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               577 gictgegtalcottalgggggggggctctctaatcaccalgaccatcatgatgaattttgcc 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 accagectgeaggaaat---egaeggggaeaggetegeegaettgeeeetaattttegat 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.8%, Score 141.2; DB 22; Length 1229; Best Local Similarity 68.4%, Pred. No. 46-23. Matches 264; Conservative 0; Mismatches 264; Conservative 0; Mismatches 269; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cell differentiation; CDIFF; agonist; antagonist; epilepsy; cell proliferation; Alzhaimar's diagease; solinsopirentic disorders; arteriosclerosis; diabetes mallitus; es;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1229 BP; 351 A; 243 C; 296 G; 339 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding CDIFF-4, Incyte ID No. 1990956CB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          637 ttatgccttgactcctgccatttatc 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
250..612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag- a //product- "CDIFF-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC85548 standard; cDNA; 1364 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC85548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
10 AAC 65546
10 AAC 65546
10 AAC 65546
10 AC 61

                     88888888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for suprthesising 5602 full-length CDMs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polymorlectide within comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at less 15 nucleotides, or (b) a combination of an oligonucleotide comprises at less 15 nucleotides.
                                                                                                                                                                     gggccatacccaataggcagatcaatgatgggatgggtggagatggagatgatatggaaa 516
                                                                                                                                                                                                                                                                                                                                              517 tattcatggaggaggaggaggaaaatcagaagaaaacttagggagctgcagtgaggaatt 576
435 ggtttggaggcaggacggtgatgaaatcaaggaaagacaggagagaagagaacagaagaaacagaaacagaace 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gictgogiatocitatgggggagcictciaatcaccaigaccaicaigatgaatitigoc 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID 10656; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         637 ttatgccttgactcctgccatttatc 662 | 1 | 1 | 1 | 1 | 1 | 1 | 543 tcataccttgaatcctaaaagttttc 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA sequence SEQ ID NO:10656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH13750 standard; cDNA; 1229 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300353.
1J-JAN-2000; 2000JP-0118776.
02-MAX-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000; 2000EP-0116126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ota T, IS
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH13750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                             00
                                                                                                                                                                                                                                         321
                                                                                                                                                                                                                                                                                                    457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          577
```

```
Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                            391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       808
 8233333333333333
                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                   쉺
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAF59590-AAF59643 represent CDRAs encoding 54 human cell cycle and proliferation proteins (crcFR), AAB6045-AB60506. CCFR and agonists of CCFR are used to treat diseases or conditions associated with decreased expression of functional CCFR. While CCFR antagonists are used to treat diseases or conditions associated with coverexpression of functional CCFR. Monoclonal or polyglonal antibodies to CCFR may be used in enzyme-linked immunosorbent assays (ELISA) or corpt may be used in enzyme-linked immunosorbent assays (ELISA) or radioimunosasys to detect CCFR. CCFR itself may be used to detect compounds of antibodies, oligonacieotides and proteins (receptors) that specifically bind to CCFPR, and in drug screening methods to
                                                                                                                                                                                                                                                                                                                                           Human cell cycle and proliferation protein CCYPR-22 cDNA, SEQ ID NO:76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cell cycle and proliferation proteins and polynucleotides are used to treat, diagnose and prevent fumme, developmental and cell signaling disorders and cell proliferative disorders including cancer.
                      577 gielgegiatectialgggggagetetetaateaealgaecateatgatgaattitgee 636
                                       637 ttatgccttgactcctgccatttatcatgagattaatactgtgattcccgctgttttctt 696
                                                                                    697 tttccttgcattttcctaatatgcctttactgatccgtttgctgtggaaccctatgttatt 756
                                                                                                                                       ggattggggaggggggtgagacagctgatggaaaagctgagggaaaagcagttgagtcata 482
                                                                                                                                                                                                                                                                                                                                                                   anagonist; que therapy; detection grotein; CCYPR; human; agonist; anagonist; que therapy; detection; gene therapy; transponist; and alsease model; limune disordar; developmental disorder; cell signalling disorder; cell proliferative disorder; cancer; tumour; anaemia, erlapsy; arterioscierosis; asthma; alterap; diabetes mellitus; menstrual cycle disorder; bacterial infection; ss.
                                                                                                                                                                        757 tocatgrateaagtgggtentgtgttgccagettetatttgaagattgcettt 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT, Yue H, Au-Young J, Bandman O;
Lu DAM, Baughn MR, Patterson C, Shah P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 181-182; 205pp; English.
                                                                                                                                                                                                                                                                 AAF59611 standard; cDNA; 898 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0145075.
99US-0153129.
99US-0164647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-2000; 2000WO-US19948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                   24-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillman JL, Lal P,
Azimzai Y, Yang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-112727/12.
P-PSDB; AAB60474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200107471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1999;
08-SEP-1999;
10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-2001.
                                                                                                                                                                                                                                                                                           AAF59611;
                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                         ò
                                                                                                                                            g
                                                                                                                                                                      ò
                                                                                                                                                                                                g
```

```
identify compounds that modulate the activity of CCYPR. CCYPR nucleotides can be used to generate transgents annial models of human disease, and can be used to generate transgents annial models of the abnormalities with respect to the expression of CGYPR for the genetic reatment or prevention of a disorder associated with CGYPR. Diseases which can be disponed, treated and prevented using CCYPR proteins, nucled caids, agonists or antagonists include immune, developmental and cell signaling disposed disporders include anneands. Specific examples of these disporders including cancer. Specific examples of these disporders disporders multiply disposed and prevents and disposed successibilities of these disporders and disposed so the menstrual cycle and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 abahacanccagababababatctcatcatggcamatattcaccaggabahcgabaga 342
264 abagagaacagagggttamacaatctcatcgtggamatgtcamccaggabahtgstgama 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343 tggagcagcctatgcagaatggagagagaaga------ccgccctttgggaggag 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              508 atatggaaatattcatggaggagagagagagagaaatcagaagaaaacttagggagctgcagt 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgagtcatagtctgcgggcagtcagcactgatccccct---caccatgaccatcacgatg 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    628 aattigocttatgocttgactccigocattatcatgagattaatactgigattccgg 687 [IIIIIIII] [IIIIIII] 621 agtittgacttatgigattcccgg 580 621 agtittcacttatgigcccggaatcctgattgigtttccccgaagttaataggagaacccgg 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttg-cactcagtgtaagtttctgtcagcagtag-tttcacccatttgcatggaaaattt 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.7%; Score 104; DB 22; Length 898;
55.4%; Pred. No. 4.9e-21;
tive 0; Mismatches 240; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtgaaggccaccagcctgcaggaaa---tcgacggggacaggctcgccgacttgccccta 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 gigaatacigigigiciagaggaaaccgiaggoggitecgegitaggeagcecatecige 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 attiticgatgggccatacccaataggcagatcaatgatgggatggtggagatggagatg 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tgaggaattgtctgcgtatccttatgggggggctctctaatcaccatgaccatcatgatg 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgittictitticettgcattitcctaatatgcctttactgatccgtttgctgtgaaccc 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     681 ttectaaacttaca------catttgtgtgtgtgtcttgtcgtaaacg 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tatgitatiticcatgigicaagigggictigigitigccagciticiatitigaagatigcci 807
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 898 BP; 250 A; 186 C; 251 G; 211 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               866 aaagccaataaagcaatttaaaaa 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                843 tcattatatattgtgaagttaata 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 55.4
Matches 346; Conservative
```

```
specification.
Sequence 862 BP; 235 A; 183 C; 238 G; 206 T; 0 other;
  ខ្ពស់
```

0 0 9 28 28 29 29 29 29 29 29 29 29 29 29 29 29 29	283 aaaacaaccagaabaaaatctcatcatgggaaatattcaccaggaaaacgaaggg 342 11 11 11 11 11 11 11	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
	tagagaangganggttaaacaatctaatogtgaaaatgtoaaccaggaaaatgatgaaa tagagacacagcattaaacaatctaatogtgaaaatgtoaaccatttgggaggag aagagaaaaggacaatgctaataaaggggaacctttggcctactttggaatgta grgaatactgtgtgctaaggaaatogaggggaaaggttogctaactttgaatgta gtgaatactgtgtgctaaggaaatogagggggaaaggttogcaatgtcccta fliii	
	tggagcagcotatgcagaatggaggaagaccgccctttgggaggag 	
	angiatgiananggagichagttgetaataanggggagecetttggecettecetttgaatgtta gtgaanggeacecagectgeaggaaa tegaeggggaeaggetegeegacttgeecet gtgaanggeacecagettggeeagaaacgtaagggggagggggggggg	
	gtgaaggcaacagcctgcaggaaa···tcgacggggacaggctcgccgacttgcccta	
	grgamartgrgtjocttaggggaaaccgtaggcggttccgcgttaggcagcccatcctgc atttccgatgggccatacccaataggcagatcaatgataggttgggtggagatgggtggg	
	atttcgatgggccatacccaataggcagatcaatgatgggtggg	~ 10 ~ 10 1
	aqtatggganattatottggggatattggggatattggggatattggggatattggggatattggggatattggggatattggggatattggggatattggggatattggggatattggggatattgggggatggggtgggattgggggtgggggtggggtgggggtgggggg	
		~ 10 .
	tgagtcatagtttgcgggcagtcagcactgatccccctcaccatgaccatcacgatg 592	~
	aattitgoottatgoottgaotootgooattatoatgagattaatactgtgattooogo 687	
	agttttgccttatgccctgaatcctgatggttccctgaagttaatagggagacccttgc 652	~
0у 688	tgtttttttttttccttgcattttcctaatatgcctttactgatccgtttgctgtgaaccc 747	_
Db 653	trectaaacttaca	
Qy 748	tatgttatttccatgigtcaagtgggtcttgtgttgccagcttctatttgaagattgcct 807	
Db 695	ttttgatgttacctatttcttgtgggtctcctattaccagcttctaaatgaatg	_
Qy 808	ttg-cactcagtgtaagtttctgtcagcagtag-tttcacccatttgcatggaaaaattt 865	ιn.
Db 755		
Qy 866	aaagccaataaagcaatttaaaaa 889	
Db 815	tcattatatattgtgaagttaata 838	

Search completed: March 11, 2002, 16:36:43 Job time: 3232 sec

```
I ALS73904 ALS73904 LTI_NPLO
BIO40889 QV3.NT0279-120201-
NW34888 RC1-DT00001-230200-
AW934905 RC1-DT00001-230200-
AW934769 RC1-DT00001-230200-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The RIKEN Genome Exploration Research Group Phase II Team and the FANKEN Genome Exploration of a full-length mouse cDNA collection
Functional annotation of a full-length mouse cDNA collection
Azakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M.,
Anakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hara, A., Hayatsu, N., Hiramoto, K., Hirawka, T.,
Miyazaki, T., Ishhi, Y., Itoh, M., Koya, S., Kurihara, C., Matsuyama, T.,
Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,
Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sana, H.,
Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, T.,
Tanaka, T., Tejima, Y., Toya, T., Yamanura, T., Yasunishi, A.,
Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genome Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1042159;
2 Jobses 1 to 789)
E 3 (bases 1 to 789)
E Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Shibata,K., Itoh,M., Aishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamanoto,H., Sakaguchi,S., Ikagami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome research. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAP trapper.

Mus musculus (strain:C57BL/6J) ES cells cDNA to mRNA,

Clone_lib:RIKEN full-length enriched mouse cDNA library

clone_1410004M13.

Mus musculus

Eukbryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Musculus;

(bases 1 to 789)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning

Methods in enzymology. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS AK010400 789 bp mRNA HTC 05-JUL-2001
DEFINITION MUS musculus ES cells cDNA, RIKEN full-length enriched library,
clone:2410004M13, full insert sequence.
ACCESSION AK010400 G1:12845816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 789)
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Ltoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genome research. 10 (10), 1617-1630 (2000)
       1182
565
668
685
662
           1.6e-23
2.0e-23
3.7e-23
3.8e-23
       586.65
584.98
580.35
580.18
       344.50
340.50
338.50
338.50
                                                                                                                                                                                                                          seq_name: gb_htc:AK010400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10349636
       gb_est1:AL573904
gb_est2:BI040889
gb_est1:AW934883
gb_est1:AW934905
gb_est1:AW934769
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Documentation | .. | Documentation | .. | Documentation | .. | AKO10400 Mus musculus ES cells | BG003261 H3086C08-5 NIA Mouse | BG003261 H3086C08-5 NIA Mouse | BE033774 us27h06.y1 Scares_NME | BE733774 us27h06.y1 Scares_NME | HE723075 mab27el2.y1 Scares_NME | HE72205 Ur.R-DVO-0ff-c-12-0 UI | AA117276 DECALLS | Scares_NME | H28956 Ur.R-DVO-0ff-c-12-0 UI | AA118340 v9112b26 Beddington mc | AA104150 mc50h03.r1 Life Tech m | W5487 mc6900.r1 | Scares mouse | AA118340 v9112b26 Beddington mc | AA107355 EST206986 Normalized r | AA107354 AV137854 Mus musculus | AA1173854 AV137854 Mus musculus | AA117389 M117899 HEMBAI Homo | BE893414 601509167PI NIH_MGC_9C | AL57301 AL57301 LTI_NFL010_LN | BE893414 AL544124 LTI_NFL006_PI | AL545120 AL542120 LTI_NFL010_EF | AL5463004 AL539004 LTI_REL013_FE | AL550650 AL56050 LTI_NFL010_EF | AL550650 AL563320 LTI_NFL010_EF | AL549875 AL5489875 LTI_NFL0012 | AL523320 AL51200120_111 | AA13855737PI NIH_MGC_59 | BG0355727PI NIH_MGC_59 | BG03556781 G025727PI NIH_MGC_59 | BG03556781 G025727PI NIH_MGC_59 | BG03556781 G025727PI NIH_MGC_59 | BG03556781999011 NIH_MGC_59 | BG03556781 G025727PI NIH_MGC_59 | BG03556781999011 NIH_MGC_59 | BG03556781 G025727PI NIH_MGC_59 | BG0355678 G0235727PI NIH_MGC_59 | BG0355727PI NIH_MGC_59 | BG0355727PI NIH_MGC_59 | BG035727PI NIH_MGC_59 | BG035727PI NIH_MGC_59 | BG035727PI NIH_MGC_59 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL582060 AL582060 LTI_NFL010_I
BI040887 QV3-NT0278-120201-502
                                                                                                                                                                                                                                                                         MODEL_frame+_p2n.model - DEV=xlh
-Q=CQ972_1/U54PO_spool/U509327750/runat_11032002_101153_20308/app_query.fasta_1.1472
-Q=CQ9702_1/U5PFO_spool/U509327750/runat_11032002_101153_20308/app_query.fasta_1.1472
-Q=CQ972_1/U5PFO_spool/U509327750/runat_11032002_101153_20308/app_query.fasta_1.1472
-Q=B=EST - OFMT=fastap -SUFFIX=ref.GAPDP=12.000 -GAPEXT=4.000
-QGAPEXT=0.000 -XGAPEXT=0.000 -XGAPEXT=0.500
-DELEXT=7.000 -YGAPCP=10.000 -XGAPEXT=0.500
-DELEXT=7.000 -START=1 -MATRIX=DOSUM62 -TRANS=human40.cdi
-LIST=45 -DCGALIGN=200 -THR_SCORE=XT-HR_ANS=100 -THR_MIN=0
-MININENO- MAXINEN-2000000000 -USR=-US09327750_eCGN1_1.5654
-NCPU-6 -ICPU-3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
                                                                                                                                                    version 4.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         software,
   out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.00 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.05 - 2.
                                                                                                                                            About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.0.0.ce
10049.004
10049.004
10041.70
937.49
937.49
937.69
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.79
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
937.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            607.78
607.47
607.29
606.94
606.89
606.61
606.46
   EST: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search information block:
Query: US-09-327-750D-35
Query length: 117
Database: EST:*
Database sequences: 11351937
Database length: 1077921985
Search time (sec): 4085.940000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6611.50
6611.50
6611.50
6611.50
6611.50
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.60
6611.6
   <u>۔</u>
of: US-09-327-750D-35
                                                                      2:16
                                                                                                                                                                                                                                              Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strd
                                                                      Date: Mar 11, 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est2:W35893
gb_est2:BF722027
gb_est2:W4487
gb_est1:AL118340
gb_est1:AN251884
gb_est1:AN251884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est2:BG083261
gb_est1:AA473525
gb_est2:BG070341
gb_est2:BF723075
gb_est1:BE333774
gb_est1:AI227867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :AI012535
:AV137854
:AA516739
:W61422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est2:BI289546
gb_est1:AA117429
gb_est2:W35893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_est2:BG527431
gb_est2:BG009563
gb_est1:AL582060
gb_est2:BI040887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est1:AL545120
qb_est2:BG709427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_estl:AL560650
gb_estl:AL539004
gb_estl:AL549875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est2:BF930215
gb_est1:AL534630
gb_est1:AL523320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE883414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_est2:BG122197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL544124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
gb_htc:AK010400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W85403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est2:W
gb_est1:A
gb_est1:A
gb_est1:A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est2:W
gb_est1:A
gb_est2:B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_estl:.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est2:
   ĕ
```

us-09-327-750d-35.rst

```
Harmonius Eucharias Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 792)

Rargul, G.J., Dudekula, D.B., Olan, Y., Lim, M.K., Jaradat, S.A., Tanaka, T.S., Carter, M.G. and Ko, M.S.H.

Verification and initial annotation of NIA mouse 15K CDNA clone set Unpublished (2001)

Verification and initial annotation of NIA mouse 15K CDNA clone set Orber_ESTS: H3086C08-3

Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdnae[graun, grc.nia.nih, gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15K.html for details.

Plate: H3086 Tow. C. column: 08
Seq primer: -21M13 Reverse
High quality sequence stop: 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Albahost-"DH10B"

//lab host-"DH10B"

//lab host-"DH10B ho
                                                                                                                                                                                                                                                                                                                                                                                                  BG083561 792 bp mRNA EST 26-JAN-2001
H3086C08-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3086C08 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
                                                                                                 /organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lone="H3086C08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG083261.1 GI:12565829
EST
                                                                                                                                                                                                                                                                                                                      seq_name: gb_est2:BG083261
                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS BG083261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLYA-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247
                                                                                                                                                                                                           116 ePro 117
                                                                                                                                                                                                                                                             558 ACCT 561
                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
                                         /translation="MASKEKQVILDLTVEKDKKDKKGKASKQSEEEPHHLEEVENKK
PGGAVRRKVRRLVPNEJMAIPNRHVDRNEGGEDVGRFVVQGTEVKRKTTEQQVRPYRR
FRTPEPDNHYDFCLIP"
770. .775
/note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/62"
/db_xref="taxon:10090"
/db_xref="MGD:MGI:1328321"
/db_xref="MGD:MGI:1308964"
/clone="241004M13"
/call=ype="ES cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 ArglysValArgArgLeuValProAsnPheLeuTrpAlalleProAsnAr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 gHisValAspArgAsnGluGlyGlyGluAspValGlyArgPheValValG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 lnGlyThrGluValLysArgLysThrThrGluGlnGlnValArgProTyr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetAlaSerLys...LysGlnValIleLeuAspLeuThrValGluLysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 1
Percent Identity: 98.305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AK010400 from: 1 to: 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAB26911.1"
/db_xref="G1:12845817"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         611.50
5.226
99.153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-327-750D-35 x AK010400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE CO
ORIGIN
```

:::

```
/Grains" BALB/C"

/ Charles" Laxon: 10090"

/ Clone="laxed: Barstead MPLRB1"

/ Sex="mixed" Barstead MPLRB1"

/ Sex="mixed" Barstead MPLRB1"

/ Sex="mixed" Barstead MPLRB1"

/ Ade_stage="6 weeks"

/ Ade_sta
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:51156 and the sequence stop: 417.

Bog primer: -28ml3 rev2 ET from Amersham and quality sequence stop: 417.

Location/Qualifiers

1. 45%

/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS BG070341 747 bp mRNA EST 26-JAN-2001
DEFINITION H3086C08-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 AGACAAAAAAGGGGGAAGGCCTCCAAACAAAGTGAAGAAGAACCCCACC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 hrGluValLysArgLysThrThrGluGlnGlnValArgProTyrArgArg 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 sAspLysArgGlyGlyLysAlaSerLysGlnSerGluGluGluProHisH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 ValArgArgLeuValProAsnPheLeuTrpAlaIleProAsnArgHisVa 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 116
Gaps: 0
Percent Identity: 97.414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AA473525 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 605.00
5.261
99.138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-327-750D-35 x AA473525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est2:BG070341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 458)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
6615el,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenstry,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS AA473525 458 bp mRNA EST 18-JUN-1997
LOCUS AA473525 ASSECTION 1978a09.rl Barstead MPLRB1 Mus musculus CDNA clone IMAGE:872056 9 similar to SW:HG74_HUWAN Q00994 OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
Contact: Marra M/Wouse EST Project
Washington University School of Medicinep
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                    489
                                                                                                                                                                                                                                                                                                                                                                                                                                  16 pLysLysAspLysArgGlyGlyLysAlaSerLysGlnSerGluGluP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 roHisHisLeuGluGluValGluAsnLysLysProGlyGlyAsnValArg 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 lnGlyThrGluValLysArgLysThrThrGluGlnGlnValArgProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 118
Gaps: 1
Percent Identity: 98.305
                                                                                                                                                                                                                                                                        to: 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                     Align seg 1/1 to: BG083261 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA473525
AA473525.1 GI:2201752
                                                                          611.50
5.226
99.153
                                                                                                                                                                                     alignment_block:
US-09-327-750D-35 x BG083261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est1:AA473525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                   Quality:
                                                                                                                         Percent Similarity:
                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540 ACCT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 ePro 117
                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
```

```
Seq primer: 40RP from Gibco
High quality sequence stop: 472.
Location/Qualifiers

1. 519

| Annual musculus |
| Annual musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Outpublished (1997).
Other_ESTS: mab27e12.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGPP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOGUS BF723075 519 bp mRNA EST 03-JAN-2001
DEFINITION mab27e12.yl Soares_NMEBA_branchial_arch Mus musculus cDNA clone
IMAGE:3971447 5' similar to TR:09Y516 09Y516 DJ63SG19.2.3 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing Musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukanyota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (Bases Lto 519)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                  531 CAAAAAAGACAAAAAGGTGGGAAGGCCTCCAAACAAAGTGAAGAAGAAC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 lnGlyThrøluValLysArgLysThrThrGluGlnGlnValArgProTyr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF723075.1 GI:12024077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est2:BF723075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS nr720775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:1471479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 ePro 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 ACCT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Jac.nost-Dialub

/Jac.nost-Dialub

clone is among a rearrayed set of 15,247 clones from 11

embryo cDNA libraries (including preimplanetation stage

embryos from unfertilized egg to blastocyst, embryonic

part of E7.5 embryos, extraembryonic part of E7.5 embryos

vand E12.5 female mesonephrosygonad) and one newborn

ovary cDNA library. Average insert size 1.5 kb. All

source libraries are cloned unidirectionally with Oligo(dT

)-Not primers. References include: (1) Genome-wide

expression profiling of mid-gestation placenta and embryo

using a 15,000 mouse developmental cDNA microarray, 2000,

Proc. Natl. Acad. Sci. U S A, 97: 912-9132; (2)

Large-scale cDNA analysis reveals phased gene expression

patterns during preimplantation mouse develolpment, 2000,

Development, 127: 1737-1749; (3) Genome-wide mapping of

unselected transcripts from extraembryonic tissue of

7.5-day mouse embryos reveals enrichment in the t-complex

and under-representation on the X chromosome, 1998, Hum

Mol Genet 7: 1967-1978.
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (2008) 1 to Judeks 1 to 74. Dudekula, D.B., Olan, Y., Lim, M.K., Jaradat, S.A., Tanaka, T.S., Carter, M.G. and Ko, M.S.H.

Verification and initial annotation of NIA mouse 15K cDNA clone set Unpublished (2001)
Other_ESTS: H3086C08-5
                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: George J. Kargul.
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Diffute on Aging/National Institutes of Health
333 Cassell Diffute, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov/cbnA/15k.html for details,
visit http://lgsun.grc.nia.nih.gov/cbNA/15k.html for details.
Plate: H3086 row: C column: 08
Plate: H3086 row: C column: 08
High quantry sequence stop: 747
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NIA Mouse 15K cDNA clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetalaSerLys...LysGlnValIleLeuAspLeuThrValGluLysAs 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLysLysAspLysArgGlyGlyLysAlaSerLysGlnSerGluGluGluP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: BG070341 from: 1 to: 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        575.50 Length: 118
5.004 Gaps: 1
97.458 Percent Identity: 96.610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .747
/organism≈"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="c57BL/6J"
/db_xref="taxon:10090"
/clone="H3086C08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host-"DH10B"
       BG070341.1 GI:12552910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-327-750D-35 x BG070341/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                libraries"
                                                                                                                     Mus musculus
                                                                              house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16
```

FEATURES

; ;;

ORIGIN

```
1. .463
//organism...wius musculus"
//db_xref="taxon:10090;
/clone="lib#cloarea_Nubba_branchial_arch"
/clone="lib#cloarea_Nubba_branchial_arch"
/clone="lib#cloarea_Nubba_branchial_arches"
/clssue_type="branchial_arches"
/clssue_type="branchial_arches"
/clssue_type="branchial_arches"
/clssue_type="branchial_arches"
/clsue_type="branchial_arches"
/clsue_type="branchial_ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
10-SEP-1996
LOCUS
W17712
W17712
DEFINITION M7712.
INAGE:335454 5' similar to SW:HG74_HUMAN 000994 OVARIAN GRANULOSA
ACCESSION W17712.
VERSION W17712.
GI:1292113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 ATGGCATCCAAATTTAAACAAGTCATACTGGATCTCACTGTGGAGAAGA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetAlaSerLys...LysGlnVallleLeuAspLeuThrValGluLysAs 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 InGlistricitvalLysArgLysThrThrGluGlnGlnValArgProTyr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 1
Percent Identity: 95.575
      image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 ArgArgPheArgThrProGluProAspAsnHisTyrAsp 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 463
                                                                        ir: -40RP from Gibco.
Location/Qualifiers
1. .463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: BE333774 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         544.50
4.950
97.345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-327-750D-35 x BE333774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est2:W17712
                                                                                          Seg primer:
                                                            MGI:1063807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:

LOCUS BEB337774

BESTATION 14-JUL-2000

DEFINITION us27h06.y1 Scares_NNEBA_branchial_arch Mus musculus cDNA clone

IMAGE:3166347 5' similar to SW:HG74_HUMAN Q00994 OVARIAN GRANULOSA

ACCESSION BE333774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musi
1 (bases 1 to 463)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 ArgLysValArgArgLeuValProAsnPheLeuTrpAlaIleProAsnAr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
                                                                                                               1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 lnGlyThrGluValLysArgLysThrThrGluGlnGlnValArgProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetAlaSerLys...LysGlnValIleLeuAspLeuThrValGluLysAs
                                                                                                                                                                                                                                                    Length: 113
Gaps: 1
Percent Identity: 96.460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ų
                                                                                                               81
                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 519
                                                                                                                  p
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: BF723075 from: 1
                                                                                                               170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE333774.1 GI:9207550
                                                                                                                  Ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                 568.50
5.168
97.345
                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-327-750D-35 x BF723075
                                                                                          Bonaldo
                                                                                                                  109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est1:BE333774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
                                                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                          Quality:
                                                                                                               158
                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
```

COMMENT

SOURCE

```
seq_documentation_block:
LOCUS A1227867 568 bp mRNA EST 20-JAN-1999
DEFINITION EST224562 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
RDRCM81 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                              Rattus sp.
Rattus sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 568)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog 6 Rat
                      AI227867.1 GI:3811754
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-327-750D-35 x AI227867/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   539.50
4.860
94.068
                                                                                                                                                                                                  seq_name: gb_est1:A1227867
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140
                                                                                                                                       117 Pro 117
                                                                                                                                                                     301 CCT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 317)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMMGE Consortium (info@image.llnl.gov) for further information.
MGI:216854
                                                                                                                                                        The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63168
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 oHisHisLeuGluGluValGluAsnLysLysProGlyGlyAsnValArgA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HisvalAspArgAsnGluGlyGlyGluAspValGlyArgPhevalvalGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 0
Percent Identity: 98.020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: W17712 from: 1 to: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541.00
5.410
99.010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-327-750D-35 x W17712
                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
              SOURCE
                                                                                                                                                          TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                       REFERENCE
                                                                                      AUTHORS
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
```

```
/clone_lib="Normalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
143 c 108 g 177 t
Unpublished (1998)
Other_ESTS: TC58086
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhieeftigr.org
Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 roHisHisLeuGluGluValGluAsnLysLysProGlyGlyAsnValArg 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: AI227867 from: 1 to: 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 1
Percent Identity: 87.288
                                                                                                                                                                                            1.568
/Organism="Rattus sp."
/db_xref="ATCC (inhost):2036891"
/db_xref="taxon:10118"
/clone="RBRCM82"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                          Location/Qualifiers
```

```
intrary is a subtracted interpred from a mixture or five individually tagged normalized rat libraries:
    brain-nRBP (20%), heart-nRHP (20%), kidney-nRKP (20%), actra-nRMP (20%), Each original library was constructed from a mixture of equal amounts of RNA from seven different developmental time-points:
    embryonic day 17, embryonic day 19, and adult day 1, adult day 12, adult day 15, and adult day 21, adult day 17, and adult day 200. (Exception: the acrta pool contains only the three embryonic stages). Each library was normalized by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the DrO subtracted individually according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the DrO subtracted library plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing the pool of libraries of about 1,000 arrayed clones from each of the five normalized libraries of brain (CTOS), heart (CSOS). Kidney (CUOS), and placenta (CNOS). The resulting pool of appresented about 2,000 arrayed clones from each of the five normalized libraries of brain (CTOS), heart (CSOS), kidney (COO), and (CTO), heart (CSO), kidney (COO), and (CTO), heart (CSO), and placenta (CNO), and CLONO content (CNO), and CNO) content (CNO), and CNO), and CNO) content (CNO) cont
      library is a subtracted library derived from a mixture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetAlaSerLys...LysGlnValIleLeuAspLeuThrValGluLysAs 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 roHisHisLeuGluGluValGluAsnLysLysProGlyGlyAsnValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 ArgLysValArgArgLeuValProAsnPheLeuTrpAlaileProAsnAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 gHisValAspArgAsnGluGlyGlyGluAspValGlyArgPheValValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 1
Percent Identity: 86.441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: BI289546 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-327-750D-35 x BI289546/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511.50
4.608
94.068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
DRIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tell 319 313 8250

Fax: 319 315 8250

Fax: 319 315 8250

Fax: 319 315 8250

Email: mscareseblue.weeg.ulowa.edu

The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized rat kidney pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through elements were found in this cDNA sequence: 1-51,

Seq Primer: Mi3 Forward

POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain-"Sprague-Dawley"
/db.xref="taxon:10116"
/db.xref="taxon:10116"
/clone="UI-R-DKO"
/clone="UI-R-DKO"
/dev_stage="ADULy"
/lab_host="Diffe Technologies"
/note="vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_I: Not I; Site_2: Eco RI; The UI-R-DKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 643)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI289546 643 bp mRNA EST 19-JUL-2001 UI-R-DKO-cff-c-12-0-UI.s1 UI-R-DKO Rattus norvegicus cDNA clone UI-R-DKO-cff-c-12-0-UI 3', mRNA sequence. BI289546.1 GI:14947228
                                                                                                                                                                                                                                                                                                                                                                                                                      83 lnGlyThrGluValLysArgLysThrThrGluGlnGlnValArgProTyr 99
                                                                                  50 ArgLysValArgArgLeuValProAsnPheLeuTrpAlaIleProAsnAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa

    . 643
    /organism="Rattus norvegicus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est2:BI289546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS B1289546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 ePro 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 ACCT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dases I to 472)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS W35893 472 bp mRNA EST 14-MAY-1996
DEFINITION mc53g09.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:352288 5' similar to SW:HG74_HUMAN Q00994 OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74. [1] ;, mRNA sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="04110B"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
WashU-HHM Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.5"
                                                                                                                                                                       66 gHisValAspArgAsnGluGlyGlyGluAspValGlyArgPheValValG 83
                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
/do_xref="taxon.10090"
/clone="IMAGE:352288"
/clone_lib="Soares mouse embryo NDME13.5
                                                                                       1 MetAlaSerLys...LysGlnValIleLeuAspLeuThrValGluLysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .472
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 441.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W35893.1 GI:1317733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: ETPrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS W35893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est2:W35893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGI:224088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 312)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moorts, M., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="embryo"
//de_stage="7.5dpc"
//de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@vatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq Priner: -40ml3 ET
                                                                                                                                                                                                                                                                                                                                     AA117429 312 bp mRNA EST 15-NOV-1996 mn21e12.rl Beddington mouse embryonic region Mus musculus cDNA clone IMAGE:538606 5' similar to SW:HG74_HUWAN Q00994 OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
Contact: Marra M/Mouse EST Project
MashU-HHMI Mouse EST Project
MashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.312...
/organism="Mus musculus"
/organism="C57BL6 x DBA"
/db_xref="taxon:10090"
/clone="IMAGE:538606"
/colone_lib="Beddington mouse embryonic region"
/sex="pooled"
Gaps: 1
Percent Identity: 98,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA117429
AA117429.1 GI:1672442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-327-750D-35 x AA117429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: AA117429
                                                                                                                                                                                                                                                 seq_name: gb_est1:AA117429
                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110
                                                                                                                        116 ePro 117
                                                                                                                                                                                     252 ACCT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
```

CDNA

```
md09c11.r1 Scares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:367892 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 GGTGGAATACAAGAAGCCTGGTGGAAATGTCCGAAGGAAAGTCAGGCGAC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 sArgLysThrThrGluGlnGlnValArgProTyrArgArgPheArgThrP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/lmage/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 uValGluAsnLysLysProGlyGlyAsnValArgArgLysValArgArgL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 GGTGGGAAGGCCTTCAATCATAGTAAAGAAGAACCCCCCCATCTGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 GlyGlyLysAlaSerLysGlnSerGluGluGluProHisLeuGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 95
Gaps: 0
Percent Identity: 93.684
                                                                 Trace considered overall poor quality
High quality sequence stop: 1
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 roGluProAspAsnHisTyrAspPheCysLeulle 116
                                                                                                                                                                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                                                                                                                                                                      58 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: BF722027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-327-750D-35 x BF722027/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W54487.1 GI:1355547
                                                                                                                                                                                                                                                                                                                                                                                                     Bonaldo."
84 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         479.00
5.207
96.842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS W54487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est2:W54487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
Mus musculus
                                                MGI:1471479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                      58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                       FEATURES
         T 3'j, on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to cloned into the Not I and Eco RI sites of the modified pr773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Ratina Bonaldo. 71 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutheria;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 286)
MCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs:r@mail.nih.gov
Contact: Robert Strausberg, M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
 BF722027 286 bp mRNA EST 03-JAN-2001 mab27e12.x1 Soares_NMEBA_branchial_arch Mus musculus cDNA clone IMAGE:3971447 3' similar to TR:Q9Y516 Q9Y516 DJ635G19.2.3 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                                                                                                                                                                                     1 MetAlaSerLys...LysGlnVallleLeuAspLeuThrValGluLysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pLysLysAspLysArgGlyGlyLysAlaSerLysGlnSerGluGluGluP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 roHisHisLeuGluGluValGluAsnLysLysProGlyGlyAsnValArg
                                                                                                                                                                                                                                                             Gaps: 1
Percent Identity: 97.938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 lnGlyThrGluValLysArgLysThrThrGluGlnGlnVal 96
                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: W35893 from: 1 to: 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF722027
BF722027.1 GI:12023029
                                                                                                                                                                                                                                           484.50
5.047
98.969
                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-327-750D-35 x W35893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est2:BF722027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS BF722027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sednence.
                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
```

COMMENT

```
318 AGAAAGIC.AGGCGACTIGIGCCTAACTTICICIGGGCCATACCAAATAG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ALDIAGET-PRINTSD-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; ist strand cDNA was primed with a Not I: Site_2: ECO RI; ist strand cDNA respected with a Not I: -oilgo(dT) primer ist strand cDNA respected with a Not I - oilgo(dT) primer ist strand cDNA respected with a Not I - oilgo(dT) primer ist strand respected with a Not I of T 3', on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 1; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatina Bonaldo.
                            1 (bases 1 to 465)
Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Tanis, M., Tanis, M., Martin, J., Morris, M., Theksing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:229324
                                                                                                                                                                            1. 465
/organism="Mus musculus"
/organism="C57BL/6J"
/db_xref="taxon:10090"
/clone="INAGE:367892"
/clone_lib="Scares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 ArgLysValArgArgLeuValProAsnPheLeuTrpAlaIleProAsnAr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469.50 Length: 99
4.840 Gaps: 1
97.980 Percent Identity: 96.970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: W54487 from: 1 to: 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mot.e.s.
Seq primer: Emprimer
High quality sequence stop: 328.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M.Fatima Bonaldo
90 c 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-327-750D-35 x W54487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                           REFERENCE
AUTHORS
                                                                                                                                                                                       TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
```

```
1. .422
/ Organism="Mus musculus"
/ Strain="(557818 musculus"
/ Strain="(557818 musculus"
/ Clone="152818 musculus"
/ Cloned musculus muscul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolation of novel tissue-specific genes from cDNA libraries representing the individual tissue constituents of the gastrulating mouse embryo
Development 121 (8), 2479-2489 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 422)
Harrison, S.M., Dunwoodie, S.L., Arkell, R.M., Lehrach, H. and
Beddington, R.S.
                                                                                                                                                                                                                                                                                                                                                                                                                        AL118340 422 bp mRNA EST 23-SEP-1999 v91121226 Beddington mouse dissected endoderm Mus musculus cDNA clone 528_13N20 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2, rue Gaston Cremieux, CP 5706, 91057 Evry CEDEX, France Email: pavner@pasteur.fr clone available from Ressourcenzentrum, Heubnerweg 6, D-14059 Berlin, Germany. Web Site http://www.rzpd.de seq primer: CCGGAATCCCGGGT.
Length: 92
Gaps: 1
Percent Identity: 98.913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Ruiz, P., Lehrach, H. and Avner, P. EEC Mouse Transcript Mapping Consortium Genoscope - CNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AL118340 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL118340.1 GI:5920179
EST ,
house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                    422 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463.50
5.093
98.913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-327-750D-35 x AL118340
                                                                                                                                                                                                                                                                                                           seq_name: gb_est1:AL118340
                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
```

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // strain="Sprague Dawley"
// db_xref="taxon:10116"
// db_xref="taxon:10116"
// clone="UI-R-BJO-adn-b-06-0-UI"
// clone="UI-R-BJO-adn-b-06-0-UI"
// db_bost="dbl10"
// db_bost="bl10"
// db_bost="dbl10"
// db_bost="dbl10"
// dbl10"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoareseblue.weeg.ulowa.edu
The sequence contained an oilgo-dr track that was present in the
oilgonucleotide that was used to prime the synthesis of first
strand coNA and therefore this may represent a bonafide poly A
trail. The sequence tag present in the cDNA between the NotI site
and the oilgo-dr track served to identify it as a clone from the
normalized atrium at 16.5 dpc library cDNA Library Preparation:
M.B. Soares Lab Clone distribution: clones will be available
through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus.
1 (bases 1 to 540)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AN251884 540 bp mRNA EST 17-DEC-1999
DEFINITION UI-R-BJO-adn-b-06-0-UI.SI UI-R-BJO Rattus norvegicus CDNA clone
UI-R-BJO-adn-b-06-0-UI 3', mRNA sequence.
50 ArgLysValArgArgLeuValProAsnPheLeuTrpAlalleProAsnAr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Rés. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 lnGlyThrGluValLysArgLysThr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW251884.1 GI:6595475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est1:AW251884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
```

```
87 lLysargLysThrThrGluGlnGlnValargProTyrargArgPheArgT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                      54 rgLeuValProAsnPheLeuTrpAlaIleProAsnArgHisValAspArg 70
                                                                                                                                                                                                                      21 ArgGlyGlyLysAlaSerLysGlnSerGluGluGluProHisHisLeuGl
                                                                                                                                                                                                 from: 1 to: 540
                                                                                                        Length: 97
Gaps: 0
Percent Identity: 86.598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 CCCCTGAACCTGACAATCATTACGACTTTTGCCTCATACCT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 hrProGluProAspAsnHisTyrAspPheCysLeuIlePro 117
6: 791-806, 1996.
TAG_LIB-UI-R-BJO
TAG_TISSUE=atrium at 16.5 dpc
                                               94 9
                                                                                                                                                                                               Align seg 1/1 to reverse of: AW251884
                                 TAG_SEQ-GATIC"
120 c
                                                                                                                                                             alignment_block:
US-09-327-750D-35 x AW251884/rev
                                                                                                                         5.044
93.814
                                                                                                            459.00
                                                                                                            Quality:
Ratio:
Percent Similarity:
                                                  146
                                                                                                   alignment_scores:
```

5652 394 394 394 4500

ĕ

```
The present invention describes primer sets for synthesising 5602

(a) an oligo-dT primer and an oligounclectide complementary

comprises: (a) an oligo-dT primer and an oligounclectide complementary

to the complementary strand of a polynuclectide which comprises one of

the 5602 nuclectide comprises at least 15 nuclectides; or (b) a combination

oligonuclectide comprises at least 15 nuclectides; or (b) a combination

of an oligonuclectide comprising a sequence complementary to the

complementary strand of a polynuclectide which comprises a 5'-end

sequence and an oligonuclectide comprising a sequence complementary to the

complementary strand of a polynuclectide which comprises a 5'-end

sequence and an oligonuclectide comprising a sequence complementary to a

polynuclectide which comprises a 3'-end sequence, where the

oligonuclectide which comprises at 15 nuclectides and the combination of

the specification. The primer sets can be used in antisense therapy and

the specification. The primers are useful for synthesising polynuclectides,

the specification and/or diagnosis of the abnormality of the full-length

complementary any specialised methods. Ash03166 to AAH13628 and

AAH3633 represent human annho acid sequences; and AAH13629 to AAH13632

complement the complement of the primers and AAH13629 to AAH13632

complementary that the complementary and are used in the exemplification
1.1e+03
2.00
2.00
2.00
46.45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs .
103.74
152.63
152.63
152.63
152.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito K, Yamamoto, Otsuki T;
   74.50
74.00
74.00
74.00
                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH03517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G; 221 T; 4 other;
/SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AA201022
/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AA12493
/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AA146784
/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AA107190
/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AA086237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 352; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashi K, S.
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA clone (5'-primer) SEQ ID NO:352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ပ်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID AAH03517 standard; cDNA; 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 239 A; 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota T, IS
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                AAH03517;
                                                                                                                                                                                                                                                                                                                                               44453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 | 2776 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 | 415 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6381
1161
1342
1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            865
1229
1364
891
                                                                                                                                                                                                                                                                             Command line parameters:
-MODEL=frame+p2n.imodel -DEV=xlh
-MODEL=frame+p2n.imodel -DEV=xlh
-MODEL=frame+p2n.imodel -DEV=xlh
-Q=/Cgn2_1/USPTQ_spool/US09327756/runat_11032002_101154_20362/app_query.fasta_1.1472
-Q=/Cgn2_1/USPTQ_spool/US09327756/runat_11032002_101154_20362/app_query.fasta_1.1472
-DB-N_Geneseq_1101 -OFMT=fastap -SUFFIX=rng -GAPOP=12.000
-GAPOT=4.500 -MOGAMEXTGH=0.000 -YGAPOF=10.000 -YGAPEXT=0.500
-GAROP=4.500 -GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -EGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DCCALIGN=200 -THR_MSCORE=pct
-TRANS=human40.cdi -LIST=45 -DCCALIGN=00 -THR_MSCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=Pfs
-USRE-USGS9323750.gCGN_1_330 -NOCPU=6 -ICQP=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.1e-34
12.7e-34
12.7e-34
12.9e-12
12.9e-12
12.6e-10
10.0039
10.0039
10.0039
10.0039
10.0039
10.0039
10.0039
10.0042
10.0042
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.00463
10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164.41
14.29
3.07
7.93
75.44
22.10
38.21
5.72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        767.81
367.98
367.98
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.79
37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Documentation 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 355.50 767.81 35
                                                                                                                                                                     About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                              out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS2/gcgdata/geneseq/geneseqn/NA2001_DAT:AAH22893
SIDS2/gcgdata/geneseq/geneseqn/NA2000_DAT:AAC38803
/SIDS2/gcgdata/geneseq/geneseqn/NA2000_DAT:AAC49751
/SIDS2/gcgdata/geneseq/geneseqn/NA1090_DAT:AAV12500
                              of: US-09-327-750D-35 to: N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/goddata/geneseq/geneseqn/NA1999./SIDS2/goddata/geneseq/geneseqn/NA1999./SIDS2/goddata/geneseq/geneseqn/NA1999./SIDS2/goddata/geneseq/geneseqn/NA1989./SIDS2/goddata/geneseq/geneseqn/NA2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search information block:
Query: US-09-377-750D-35
Query length: 117
Database: N_Geneseq_1101:*
Database sequences: 930621
Database length: 428662619
Search time (sec): 355.560000
                                                                                                    Date: Mar 11, 2002 3:42
```